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Hatzfeld et al.

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(54) **RICE PROMOTERS**

(75) Inventors: **Yves Hatzfeld**, Lille (FR); **Willem Broekaert**, Dilbeek (BE)

(73) Assignee: **Crop Design N.V.** (BE)

(*) Notice: Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 0 days.

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(65) **Prior Publication Data**

US 2013/0007914 A1 Jan. 3, 2013

Related U.S. Application Data

(62) Division of application No. 12/229,130, filed on Aug. 20, 2008, which is a division of application No. 10/525,647, filed as application No. PCT/EP2004/050081 on Feb. 4, 2004, now Pat. No. 7,427,676.

(30) **Foreign Application Priority Data**

Feb. 4, 2003 (EP) 03075331

(51) **Int. Cl.**
C12N 15/82 (2006.01)
C12N 15/87 (2006.01)

(52) **U.S. Cl.**
CPC ***C12N 15/8234*** (2013.01); ***C12N 15/8216*** (2013.01); ***C12N 15/8222*** (2013.01)
USPC **800/287**; 536/24.1; 800/278; 435/320.1

(58) **Field of Classification Search**
USPC 800/287
See application file for complete search history.

(56) **References Cited**

U.S. PATENT DOCUMENTS

2007/0020621 A1* 1/2007 Boukharov et al. 435/6

* cited by examiner

Primary Examiner — Li Zheng
(74) *Attorney, Agent, or Firm* — Barbara E. Johnson, Esq.

(57) **ABSTRACT**

The invention provides several promoters isolated from *Oryza sativa*, which promoters are capable of driving and/or regulating the expression of an operably linked nucleic acid in a plant. The expression patterns of the promoters according to the invention have been studied in *Oryza sativa* and some of the promoters displayed specific activity in particular cells, tissues or organs of the plant, while others displayed constitutive expression throughout substantially the whole plant. Some promoters showed weak expression, while others were strongly active.

3 Claims, 11 Drawing Sheets

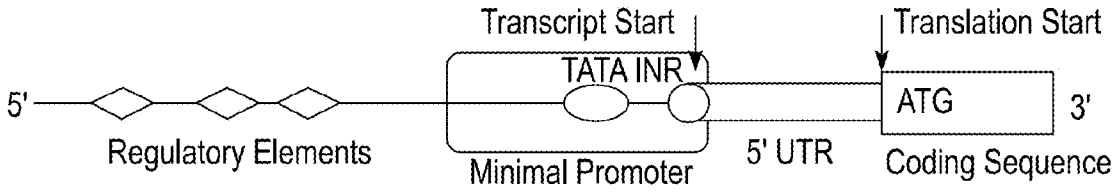


FIGURE 1

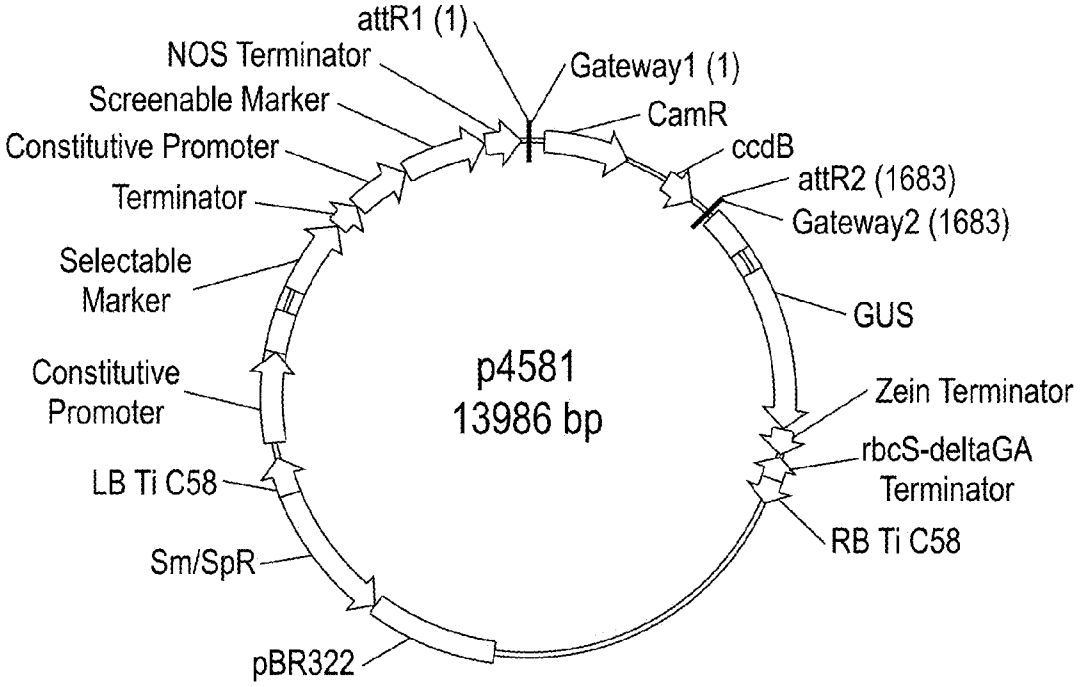


FIGURE 2

PRO0110 RCc3

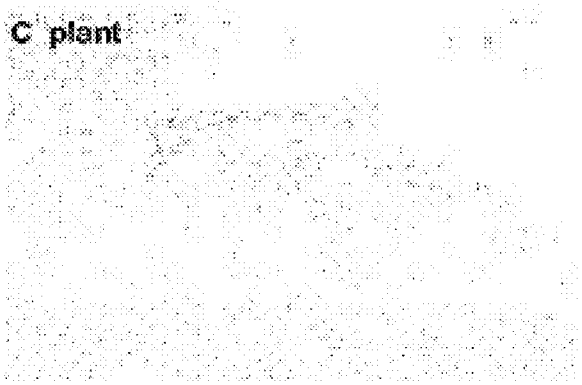


FIGURE 3

PRO0005 putative beta-amylase

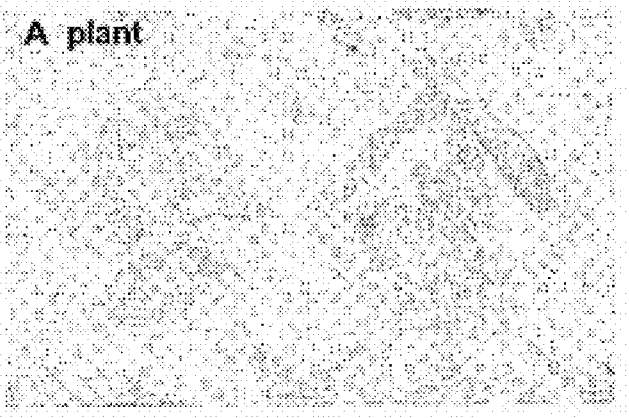


FIGURE 4

PRO0009 putative cellulose synthase

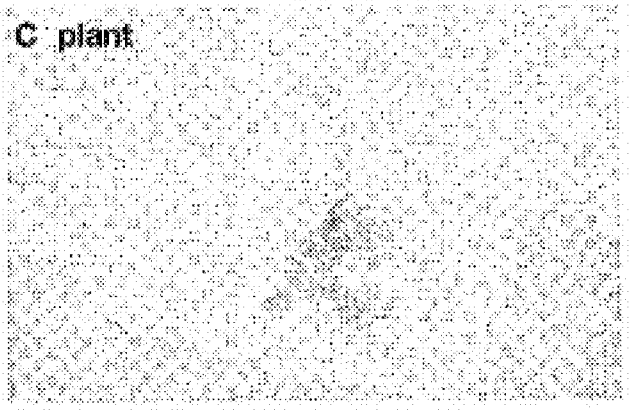


FIGURE 5

PRO058 proteinase inhibitor Rgpi9

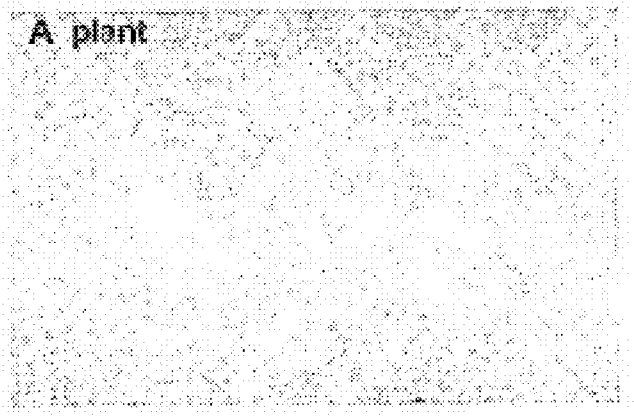
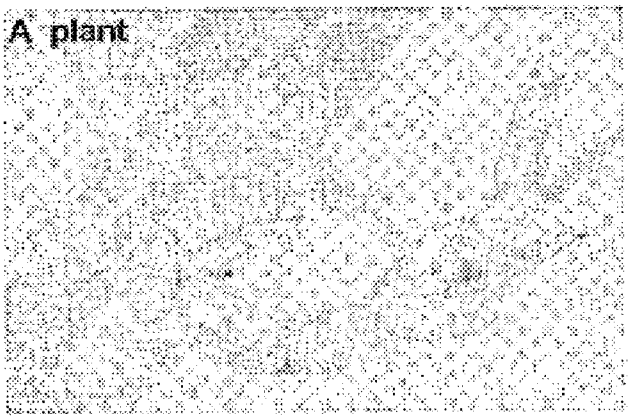


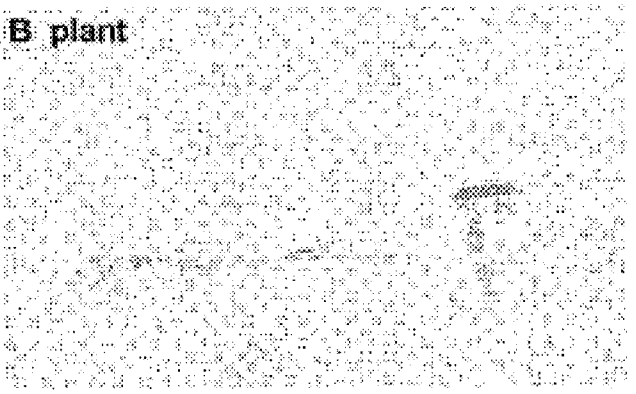
FIGURE 6

PRO061 beta-expansion EXPB9

A



B



C

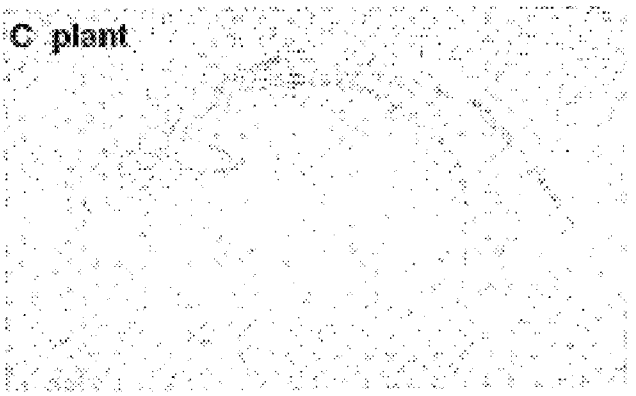
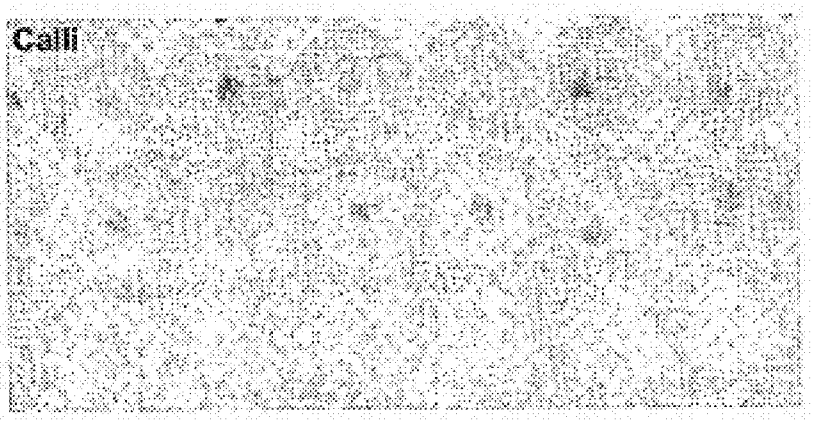


FIGURE 7

PRO0063 structural protein

A



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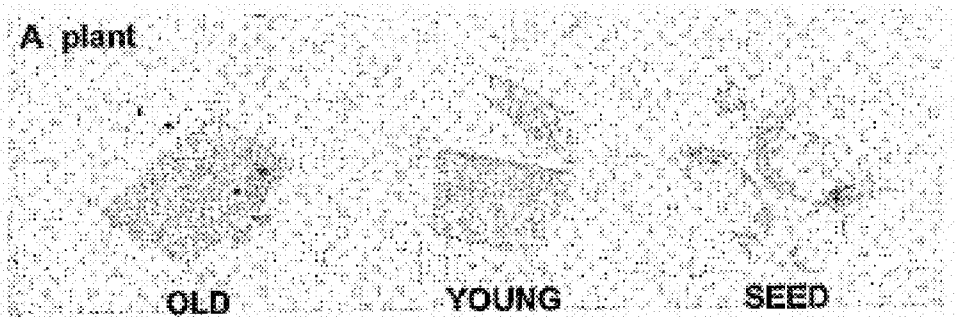


FIGURE 8

PRO0081 putative caffeoyl CoA 3-O-methyltransferase

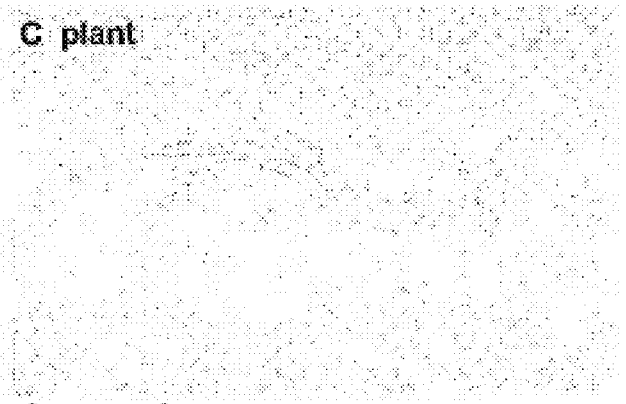
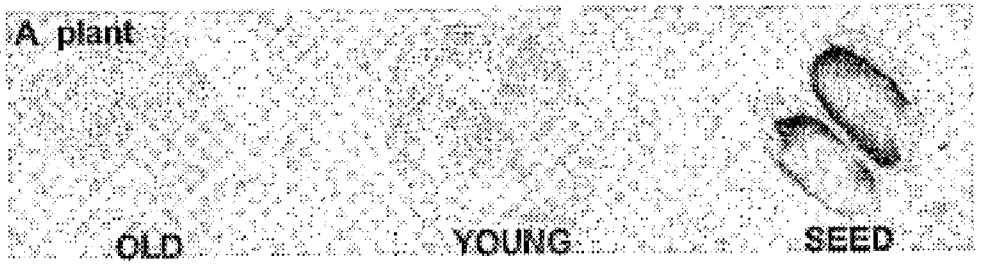


FIGURE 9

PRO0091 prolamin RP5

A



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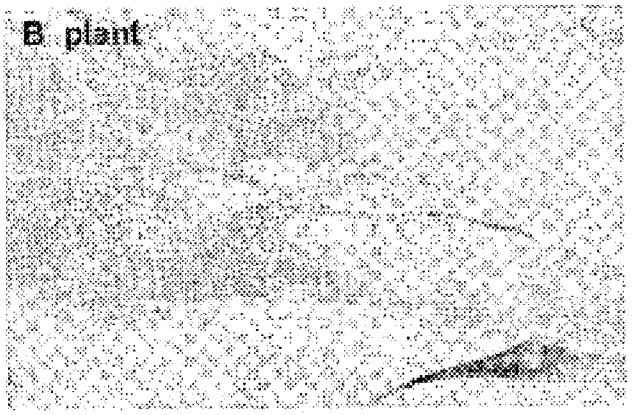


FIGURE 10

PRO0095 putative methionine aminopeptidase

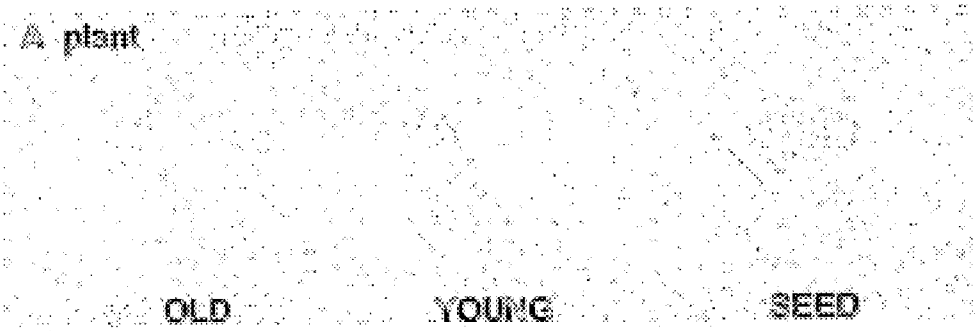


FIGURE 11

PRO0111 uclacyanin 3-like protein

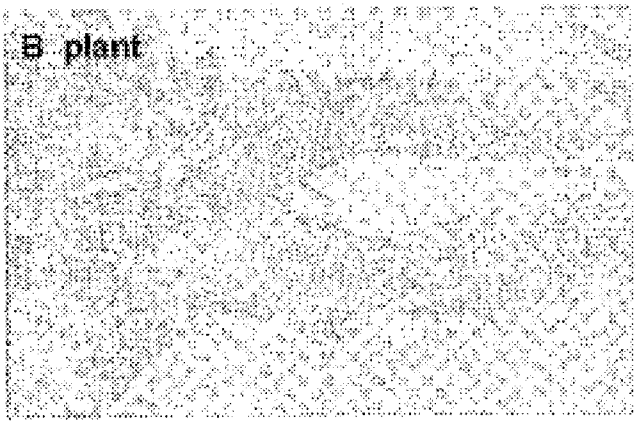


FIGURE 12

PRO0116 26S proteaseome regulatory particle non-ATPase subunit 11

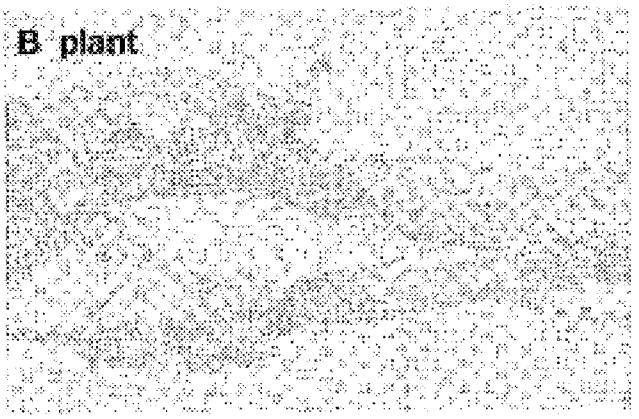


FIGURE 13

PRO0117 putative 40S ribosomal protein

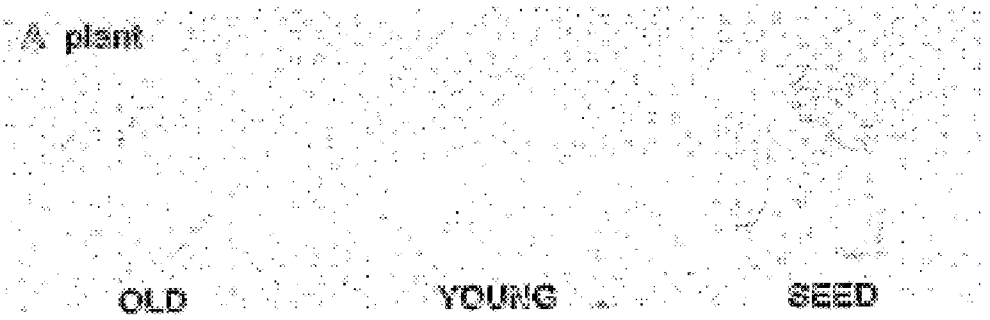


FIGURE 14

PRO0122 chlorophyll a/b binding protein precursor (Cab27)

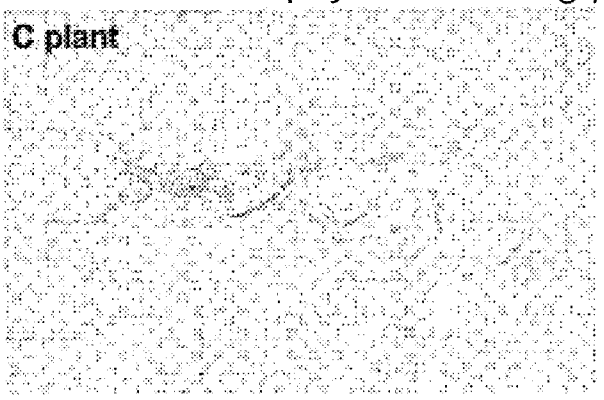


FIGURE 15

PRO0123 putative protochlorophyllide reductase

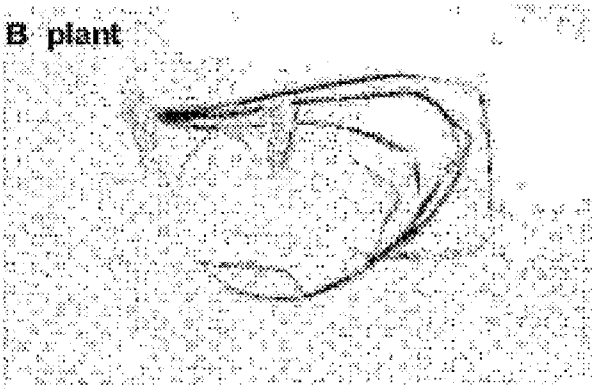


FIGURE 16

PRO0133 chitinase Cht-3

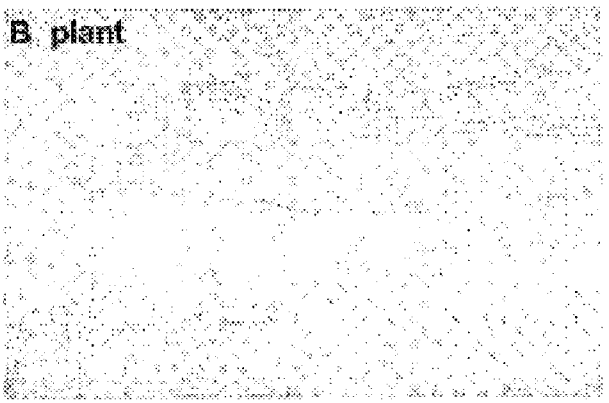
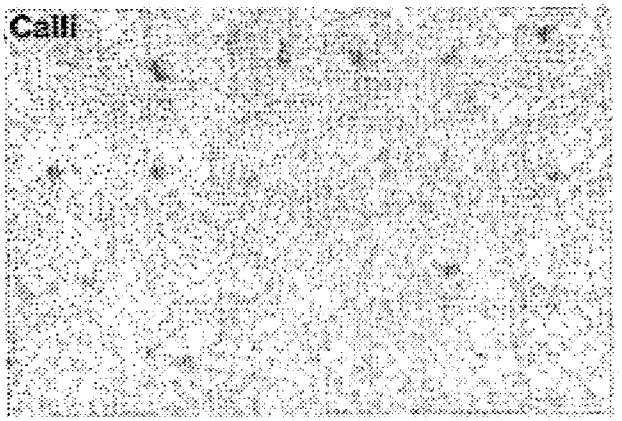


FIGURE 17

PRO01151 WSI18

A Calli



B Seed

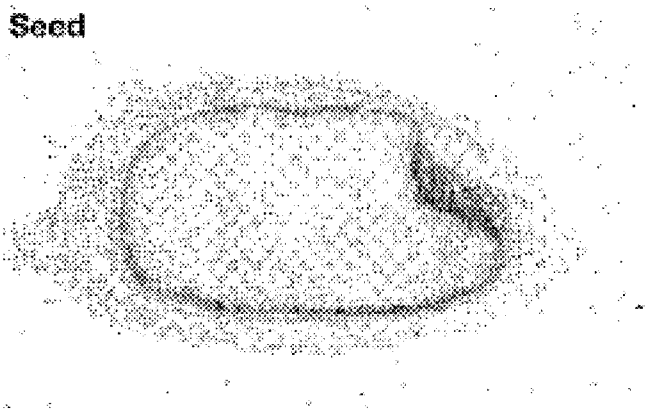


FIGURE 18

PRO0169 acquaporine

C plant

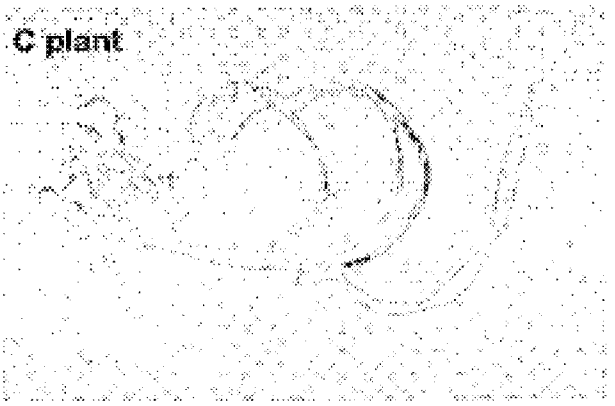
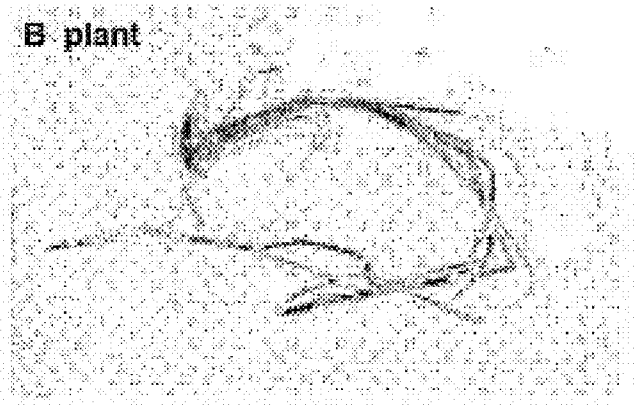


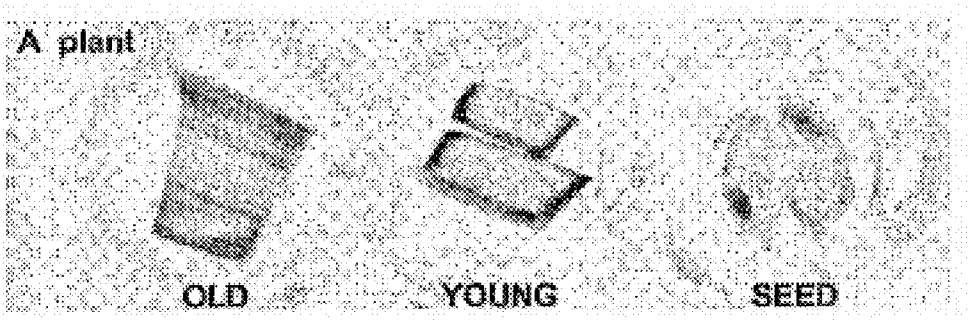
FIGURE 19

PRO0170 high mobility group protein

A B plant



B A plant



C Calli

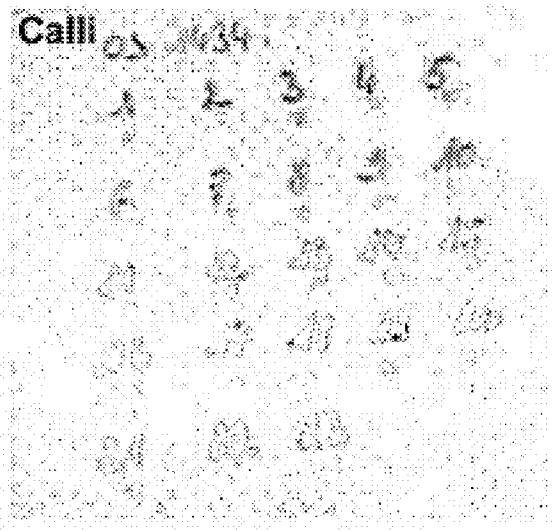


FIGURE 20

PRO0171 reversibly glycosylated protein RGP1

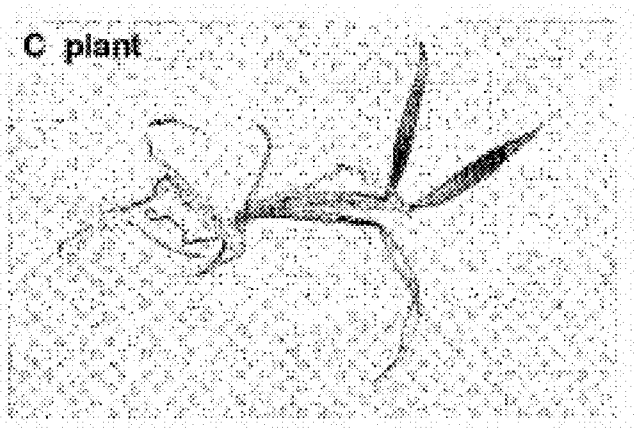


FIGURE 21

PRO0173 cytosolic MDH

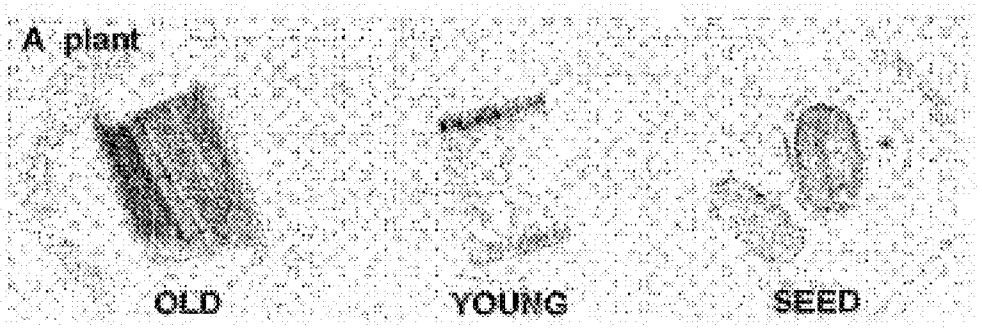
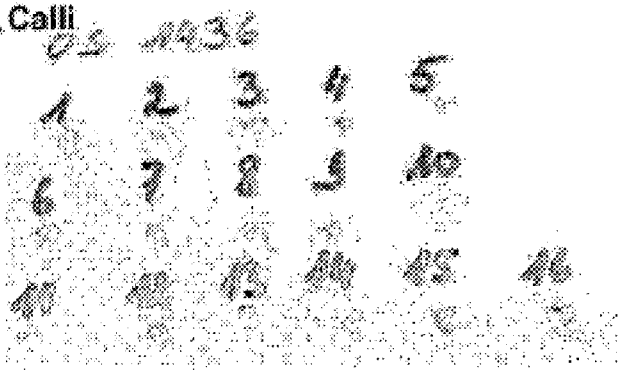


FIGURE 22

PRO0175 RAB21

A Calli



B Seed

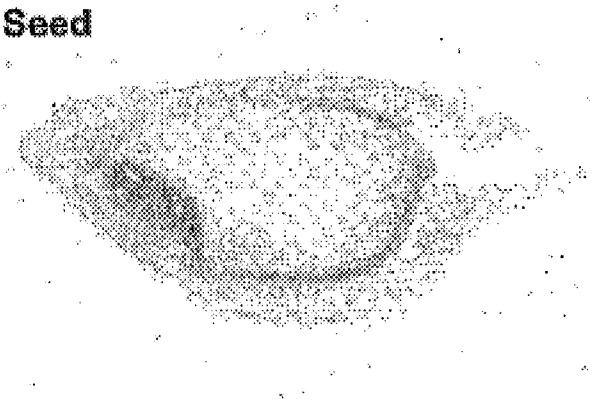


FIGURE 23

PRO0177 Cdc2-1

C plant

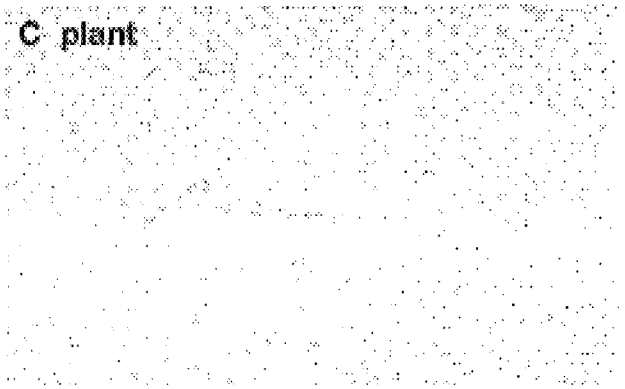


FIGURE 24

RICE PROMOTERS

CROSS-REFERENCE TO RELATED APPLICATIONS

The present patent application claims priority and forms part of a chain of continuing applications as follows: the present application, U.S. Ser. No. 13/471,930, filed 15 May 2012, is a division U.S. Ser. No. 12/229,130 filed 20 Aug. 2008, which is a division of U.S. Ser. No. 10/525,647 filed 24 Feb. 2005, now U.S. Pat. No. 7,427,676, which is a Section 371 U.S. application based upon international application number PCT/EP04/50081 filed 4 Feb. 2004, which claims priority to EPO 03075331.3 filed 4 Feb. 2003, each of which is incorporated herein by reference.

The present invention relates to the field of plant molecular biology, more particularly to nucleic acid sequences useful for driving and/or regulating expression of an operably linked nucleic acid in plants. The isolation of these nucleic acid sequences from rice, as well as their use in driving and/or regulating expression of an operably linked nucleic acid is disclosed. The present invention therefore concerns promoters, hybrid promoters, genetic constructs, expression cassettes, transformation vectors, expression vectors, host cells and transgenic plants comprising the isolated nucleic acids according to the present invention. The present invention also concerns methods for driving and/or regulating expression of a nucleic acid and methods for the production of transgenic plants.

Gene expression is dependent on initiation of transcription, which is mediated via the transcription initiation complex. Gene expression is also dependent on regulation of transcription, which regulation determines how strong, when or where a gene is expressed. Said regulation of gene expression may be mediated via transcriptional control elements, which are generally embedded in the nucleic acid sequence 5'-flanking or upstream of the expressed gene. This upstream nucleic acid region is often referred to as a "promoter" since it promotes the binding, formation and/or activation of the transcription initiation complex and therefore is capable of driving and/or regulating expression of the 3' downstream nucleic acid sequence.

Genetic engineering of plants with the aim of obtaining a useful plant phenotype, often involves heterologous gene expression, which is generally mediated by a promoter capable of driving and/or regulating expression of an operably linked heterologous nucleic acid. The phenotype of the host plant only depends on the contribution of the heterologous nucleic acid, but also on the contribution of the specific expression pattern of the chosen promoter determining how, where and when that heterologous nucleic acid is expressed. Accordingly, the choice of promoter with a suitable expression pattern is of crucial importance for obtaining the suitable phenotype. A person skilled in the art will need to have available different promoters, to determine the optimal promoter for a particular nucleic acid. For many different host plants, this availability is rather limited and there is therefore a continuing need to provide new promoters with various expression profiles.

The nucleic acids as presented in SEQ ID NO 1 to 22 were isolated from *Oryza sativa* and have been found to be capable of driving and regulating expression of an operably linked nucleic acid; their expression patterns have also been characterized. Therefore the present invention offers a collection of hitherto unknown isolated nucleic acids, which isolated nucleic acids are useful as promoters.

Accordingly, the present invention provides an isolated promoter capable of driving and/or regulating expression, comprising:

(a) an isolated nucleic acid as given in any one of SEQ ID NO 1 to 22 or the complement of any one of SEQ ID NO 1 to 22; or

(b) an isolated nucleic acid having at least 90% sequence identity with any of the DNA sequences as given in any one of SEQ ID NO 1 to 22; or

(c) an isolated nucleic acid specifically hybridizing under stringent conditions with any of the DNA sequences as given in any one of SEQ ID NO 1 to 22; or

(d) an isolated nucleic acid as defined in any one of (a) to (c), which is interrupted by an intervening sequence; or

(e) a fragment of any of the nucleic acids as defined in (a) to (d), which fragment is capable of driving and/or regulating expression.

The term "isolated" as used herein means being removed from its original source. Preferably, the "isolated" promoter is free of sequences (such as protein encoding sequences or other sequences at the 3' end) that naturally flank the promoter in the genomic DNA of the organism from which the promoter is derived. Further preferably, the "isolated" promoter is also free of sequences that naturally flank it at the 5' end. Further preferably, the "isolated" promoter may comprise less than about 5 kb, 4 kb, 3 kb, 2 kb, 1.5 kb, 1.2 kb, 1 kb, 0.8 kb, 0.5 kb or 0.1 kb of nucleotide sequences that naturally occur with the promoter in genomic DNA from the organism of which the promoter is derived.

The present invention is not limited to the nucleic acids as presented by SEQ ID NO 1 to 22. A person skilled in the art will recognize that variants or fragments of a nucleic acid may occur, whilst maintaining the same functionality. These variants or fragments may be man made (e.g. by genetic engineering) or may even occur in nature. Therefore the present invention extends to variant nucleic acids and fragments of any of SEQ ID NO 1 to 22, which variants or fragments are useful in the methods of the present invention. Such variants and fragments include:

(a) an isolated nucleic acid as given in any one of SEQ ID NO 1 to 22 or the complement of any one of SEQ ID NO 1 to 22; or

(b) an isolated nucleic acid having at least 90% sequence identity with any of the DNA sequences as given in any one of SEQ ID NO 1 to 22; or

(c) an isolated nucleic acid specifically hybridizing under stringent conditions with any of the DNA sequences as given in any one of SEQ ID NO 1 to 22; or

(d) an isolated nucleic acid as defined in any one of (a) to (c), which is interrupted by an intervening sequence; or

(e) a fragment of any of the nucleic acids as defined in (a) to (d), which fragment is capable of driving and/or regulating expression.

Suitable variants of any one of SEQ ID NO 1 to 22 encompass homologues which have in increasing order of preference at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity with any one of the nucleic acids as represented in SEQ ID NO 1 to 22.

The percentage of identity may be calculated using an alignment program. Preferably a pair wise global alignment program may be used, which implements the algorithm of Needleman-Wunsch (J. Mol. Biol. 48: 443-453, 1970). This algorithm maximizes the number of matches and minimizes the number of gaps. Such programs are for example GAP, Needle (EMBOSS package), stretcher (EMBOSS package) or Align X (Vector NTI suite 5.5) and may use the standard parameters (for example gap opening penalty 15 and gap

extension penalty 6.66). Alternatively, a local alignment program implementing the algorithm of Smith-Waterman (Advances in Applied Mathematics 2, 482-489 (1981)) may be used. Such programs are for example Water (EMBOSS package) or matcher (EMBOSS package). "Sequence identity" as used herein is preferably calculated over the entire length of the promoters as represented by any one of SEQ ID NO 1 to 22. The length of these promoters is presented in Table 2.

Search and identification of homologous nucleic acids, would be well within the realm of a person skilled in the art. Such methods involve screening sequence databases with the sequences provided by the present invention, for example any one of SEQ ID NO 1 to 22, preferably in a computer readable form. Useful sequence databases include but are not limited to Genbank, the European Molecular Biology Laboratory Nucleic acid Database (EMBL) or versions thereof, or the MIPS database. Different search algorithms and software for the alignment and comparison of sequences are well known in the art. Such software includes, for example GAP, BESTFIT, BLAST, FASTA and TFASTA. Preferably BLAST software is used, which calculates percent sequence identity and performs a statistical analysis of the similarity between the sequences. The suite of programs referred to as BLAST programs has 5 different implementations: three designed for nucleotide sequence queries (BLASTN, BLASTX, and TBLASTX) and two designed for protein sequence queries (BLASTP and TBLASTN) (Coulson, Trends in Biotechnology: 76-80, 1994; Birren et al., GenomeAnalysis, 1: 543, 1997). The software for performing BLAST analysis is publicly available through the National Centre for Biotechnology Information.

The sequences of the genome of *Arabidopsis thaliana* and the genome of *Oryza sativa* are now available in public databases such as Genbank. Other genomes are currently being sequenced. Therefore, it is expected that as more sequences of the genomes of other plants become available, homologous promoters may be identifiable by sequence alignment with any one of SEQ ID NO 1 to SEQ ID NO 22. The skilled person will readily be able to find homologous promoters from other plant species, for example from other crop plants, such as maize. Homologous promoters from other crop plants are especially useful for practising the methods of the present invention in crop plants.

One example of homologues having at least 90% sequence identity with any one of SEQ ID NO to 22 are allelic variants of any one of SEQ ID NO 1 to 22. Allelic variants are variants of the same gene occurring in two different individuals of the same species and usually allelic variants differ by slight sequence changes. Allelic variants may encompass Single Nucleotide Polymorphisms (SNPs) as well as Small Insertion/Deletion Polymorphisms (INDELs). The size of INDELs is usually less than 100 bp. SNPs and INDELs form the largest set of sequence variants in naturally occurring polymorphic strains of most organisms.

Homologues suitable for use in the methods according to the invention may readily be isolated from their source organism via the technique of PCR or hybridization. Their capability of driving and/or regulating expression may readily be determined, for example, by following the methods described in the Examples section by simply substituting the sequence used in the actual Example with the homologue.

Other suitable variants of any one of SEQ ID NO 1 to 22 encompassed by the present invention are nucleic acids specifically hybridising under stringent conditions to any one of the nucleic acids of SEQ ID NO 1 to 22. The term "hybridising" means annealing to substantially homologous complementary nucleotide sequences in a hybridization process. Tools in molecular biology relying on such a hybridization process include the polymerase chain reaction (PCR; and all methods based thereon), subtractive hybridisation, random primer extension, nuclease S1 mapping, primer extension, reverse transcription, cDNA synthesis, differential display of RNAs, and DNA sequence determination, Northern blotting (RNA blotting), Southern blotting (DNA blotting). The hybridisation process can also occur with one of the complementary nucleic acids immobilised to a matrix such as magnetic beads, Sepharose beads or any other resin. Tools in molecular biology relying on such a process include the isolation of poly (A+) mRNA. The hybridisation process can furthermore occur with one of the complementary nucleic acids immobilised to a solid support such as a nitro-cellulose or nylon membrane or immobilised by e.g. photolithography to, for example, a siliceous glass support (the latter known as nucleic acid arrays or microarrays or as nucleic acid chips). Tools in molecular biology relying on such a process include RNA and DNA gel blot analysis, colony hybridisation, plaque hybridisation, in situ hybridisation and microarray hybridisation. In order to allow hybridisation to occur, the nucleic acid molecules are generally thermally or chemically denatured to melt a double strand into two single strands and/or to remove hairpins or other secondary structures from single stranded nucleic acids. The stringency of hybridisation is influenced by conditions such as temperature, salt concentration and hybridisation buffer composition. Conventional hybridisation conditions are described in, for example, Sambrook (2001) Molecular Cloning: a laboratory manual, 3rd Edition Cold Spring Harbor Laboratory Press, CSH, New York, but the skilled craftsman will appreciate that numerous different hybridisation conditions can be designed in function of the known or the expected homology and/or length of the nucleic acid sequence. High stringency conditions for hybridisation include high temperature and/or low sodium/salt concentration (salts include sodium as for example in NaCl and Na_3-citrate) and/or the inclusion of formamide in the hybridisation buffer and/or lowering the concentration of compounds such as SDS (sodium dodecyl sulphate detergent) in the hybridisation buffer and/or exclusion of compounds such as dextran sulphate or polyethylene glycol (promoting molecular crowding) from the hybridisation buffer. Specifically hybridising under stringent conditions means that the sequences have to be very similar. Specific hybrisization under stringent conditions is preferably carried out at a temperature of 60° C. followed by washes in 0.1 to 1×SSC, 0.1×SDS, and 1×SSC, 0.1×SDS.

The invention also relates to a nucleic acid molecule of at least 15 nucleotides in length hybridizing specifically with any of the nucleic acids of the invention. The invention also relates to a nucleic acid molecule of at least 15 nucleotides in length specifically amplifying a nucleic acid of the invention by polymerase chain reaction.

Another variant of any of SEQ ID NO 1 to 22 encompassed by the present invention are nucleic acids corresponding to any one of SEQ ID NO 1 to 22 or variants thereof as described hereinabove, which are interrupted by an intervening sequence. For example, any of the nucleic acids as presented in SEQ ID NO 1 to 22 may be interrupted by an intervening sequence. With "intervening sequences" is meant any nucleic acid or nucleotide, which disrupts another sequence. Examples of intervening sequences comprise introns, nucleic acid tags, T-DNA and mobilizable nucleic acids sequences such as transposons or nucleic acids that can be mobilized via recombination. Examples of particular transposons comprise Ac (activator), Ds (Dissociation), Spm (suppressor-Mutator) or En. The introduction of introns into promoters is now

widely applied. The methods according to the present invention may also be practised using a nucleic acid sequence according to any one of SEQ ID NO 1 to 22 provided with an intron. In case the intervening sequence is an intron, alternative splice variants of the nucleic acids according to the invention may arise. The term "alternative splice variant" as used herein encompasses variants of a nucleic acid sequence in which intervening introns have been excised, replaced or added. Such splice variants may be found in nature or may be manmade. Methods for making such promoters with an intron or for making the corresponding splice variants are well known in the art.

Variants interrupted by an intervening sequence, suitable for use in the methods according to the invention may readily be determined for example by following the methods described in the Examples section by simply substituting the sequence used in the actual Example with the variant.

The variant nucleic acids as described hereinabove may be found in nature (for example allelic variants or splice variants). Additionally and/or alternatively, variants of any one of SEQ ID NO 1 to 22 as described hereinabove may be manmade via techniques well known in the art involving for example mutation, substitution, insertion, deletions or derivation. The present invention also encompasses such variants, as well as their use in the methods of the present invention.

A "mutation variant" of a nucleic acid may readily be made using recombinant DNA manipulation techniques or nucleotide synthesis. Examples of such techniques include site directed mutagenesis via M13 mutagenesis, T7-Gen in vitro mutagenesis (USB, Cleveland, Ohio), QuickChange Site Directed mutagenesis (Stratagene, San Diego, Calif.), PCR-mediated site-directed mutagenesis or other site-directed mutagenesis protocols. Alternatively, the nucleic acid of the present invention may be randomly mutated.

A "substitutional variant" refers to those variants in which at least one residue in the nucleic acid sequence has been removed and a different residue inserted in its place. Nucleic acid substitutions are typically of single residues, but may be clustered depending upon functional constraints placed upon the nucleic acid sequence; insertions usually are of the order of about 1 to about 10 nucleic acid residues, and deletions can range from about 1 to about 20 residues.

An "insertional variant" of a nucleic acid is a variant in which one or more nucleic acid residues are introduced into a predetermined site in that nucleic acid. Insertions may comprise 5'-terminal and/or 3'-terminal fusions as well as intra-sequence insertions of single or multiple nucleotides. Generally, insertions within the nucleic acid sequence will be smaller than 5'- or 3'-terminal fusions, of the order of about 1 to 10 residues. Examples of 5'- or 3'-terminal fusions include the coding sequences of binding domains or activation domains of a transcriptional activator as used in the yeast two-hybrid system or yeast one-hybrid system, or of phage coat proteins, $(histidine)_6$-tag, glutathione S-transferase-tag, protein A, maltose-binding protein, dihydrofolate reductase, Tag●100 epitope, c-myc epitope, FLAG®-epitope, lacZ, CMP (calmodulin-binding peptide), HA epitope, protein C epitope and VSV epitope.

The term "derivative" of a nucleic acid may comprise substitutions, and/or deletions and/or additions of naturally and non-naturally occurring nucleic acid residues compared to the natural nucleic acid. Derivatives may, for example, comprise methylated nucleotides, or artificial nucleotides.

Also encompassed with in the present invention are promoters, comprising a fragment of any of the nucleic acids as presented by any one of SEQ ID NO 1 to 22 or variants thereof as described hereinabove. A "fragment" as used herein means a portion of a nucleic acid sequence. Suitable fragments useful in the methods of the present invention are functional fragments, which retain at least one of the functional parts of the promoter and hence are still capable of driving and/or regulating expression. Examples of functional fragments of a promoter include the minimal promoter, the upstream regulatory elements, or any combination thereof.

Suitable fragments may range from at least about 20 base pairs or about 50, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950 or 1000 base pairs, up to about the full length sequence of the invention. These base pairs are typically immediately upstream of the transcription initiation start, but alternatively may be from anywhere in the promoter sequence.

Suitable fragments useful in the methods of the present invention may be tested for their capability of driving and/or regulating expression by standard techniques well known to the skilled person, or by the following method described in the Example section.

The promoters as disclosed in any one of SEQ ID NO 1 to 22 are isolated as nucleic acids of approximately 1.2 kb from the upstream region of particular rice coding sequences (CDS). These nucleic acids may include typical elements of a promoter, which are presented in FIG. **1**. Generally, a promoter may comprises from coding sequence to the upstream direction: (i) an 5'UTR of pre-messenger RNA, (ii) a minimal promoter comprising the transcription initiation element (INR) and more upstream a TATA box, and (iii) may contain regulatory elements that determine the specific expression pattern of the promoter.

The term "promoter" as used herein is taken in a broad context and refers to regulatory nucleic acid sequences capable of effecting (driving and/or regulating) expression of the sequences to which they are operably linked. A "promoter" encompasses transcriptional regulatory sequences derived from a classical genomic gene. Usually a promoter comprises a TATA box, which is capable of directing the transcription initiation complex to the appropriate transcription initiation start site. However, some promoters do not have a TATA box (TATA-less promoters), but are still fully functional for driving and/or regulating expression. A promoter may additionally comprise a CCAAT box sequence and additional regulatory elements (i.e. upstream activating sequences or cis-elements such as enhancers and silencers). A "promoter" may also include the transcriptional regulatory sequences of a classical prokaryotic gene, in which case it may include a −35 box sequence and/or a −10 box transcriptional regulatory sequences.

"Driving expression" as used herein means promoting the transcription of a nucleic acid.

"Regulating expression" as used herein means influencing the level, time or place of transcription of a nucleic acid. The promoters of the present invention may thus be used to increase, decrease or change in time and/or place transcription of a nucleic acid. For example, they may be used to limit the transcription to certain cell types, tissues or organs, or during a certain period of time, or in response to certain environmental conditions.

The promoter is preferably a plant-expressible promoter. The term "plant-expressible" means being capable of regulating expression in a plant, plant cell, plant tissue and/or plant organ. Accordingly, the invention encompasses an isolated nucleic acid as mentioned above, capable of regulating transcription of an operably linked nucleic acid in a plant or in one or more particular cells, tissues or organs of a plant.

The expression pattern of the promoters according to the present invention were studied in detail and it was found that

many of them were tissue-specific. Accordingly, the present invention provides "tissue-specific" promoters. The term "tissue-specific" shall be taken to indicate that expression is predominantly in a particular tissue, tissue-type, organ or any other part of the organism, albeit not necessarily exclusively in said tissue, tissue-type, organ or other part. Accordingly, the invention encompasses an isolated nucleic acid as mentioned above, capable of driving and/or regulating expression (of an operably linked nucleic acid) in a tissue-specific manner. Expression may be driven and/or regulated in the seed, embryo, scutellum, aleurone, endosperm, leaves, flower, calli, meristem, shoot meristem, discriminating centre, shoot, shoot meristem and root. In grasses the shoot meristem is located in the so-called discrimination zone from where the shoot and the leaves originate.

A tissue-specific promoter is one example of a so-called "regulated promoter". These promoters are regulated by endogenous signals such as the presence of certain transcription factors, metabolites, plant hormones, or exogenous signals, such as ageing, stresses or nutritional status. These regulations may have an effect on one or more different levels such spatial specificity or temporal specificity. Encompassed within the present invention is a nucleic acid as described hereinabove, which is a "regulated promoter". Examples of regulated promoters are cell-specific promoters, tissue-specific promoters, organ-specific promoters, cell cycle-specific promoters, inducible promoters or young tissue-specific promoters.

Alternatively and/or additionally, some promoters of the present invention display a constitutive expression pattern. Accordingly, the present invention provides a promoter as described hereinabove, which is a constitutive promoter. The term "constitutive" means having no or very few spatial or temporal regulations. The term "constitutive expression" as used herein refers to a substantially continuously expression in substantially all tissues of the organism. The skilled craftsman will understand that a "constitutive promoter" is a promoter that is active during most, but not necessarily all, phases of growth and development of the organism and throughout most, but not necessarily all, parts of an organism.

The "expression pattern" of a promoter is not only influenced by the spatial and temporal aspects, but also by the level of expression. The level of expression is determined by the so-called "strength" of a promoter. Depending on the resulting expression level, a distinction is made herein between "weak" or "strong" promoters. Generally by "weak promoter" is meant a promoter that drives expression of an operably linked nucleic acid at levels of about $1/10000$ transcripts to about $1/100000$ transcripts to about $1/500000$ transcripts. Generally, by "strong promoter" is meant a promoter that drives expression at levels of about $1/10$ transcripts, to about $1/100$ or to about $1/1000$ transcripts.

According to a particular embodiment, the invention provides an isolated promoter as mentioned hereinabove, which is a hybrid promoter. The term "hybrid promoter" as used herein refers to a chimeric promoter made, for example, synthetically, for example by genetic engineering. Preferred hybrid promoters according to the present invention comprise a part, preferably a functional part, of one of the promoters according to the present invention and at least another part, preferably a functional part of a promoter. The latter part, may be a part of any promoter, including any one of the promoters according to the present invention and other promoters. One example of a hybrid promoter comprises regulatory element(s) of a promoter according to the present invention combined with the minimal promoter of another promoter. Another example of a hybrid promoter is a promoter comprising additional regulatory elements to further enhance its activity and/or to alter its spatial and/or temporal expression pattern.

The present invention also provides use of a functional fragment of any one of SEQ ID NO 1 to 22 or variant thereof for changing the expression pattern of a promoter. In such methods, at least part of any of the nucleic acids according to the present invention are combined with at least one fragment of another promoter.

Further, the invention provides a genetic construct comprising:

(a) An isolated promoter as defined hereinabove

(b) A heterologous nucleic acid sequence operably linked to isolated promoter of (a), and optionally

(c) A 3' transcription terminator

The term "genetic construct" as used herein means a nucleic acid made by genetic engineering.

The term "operably linked" to a promoter as used herein means that the transcription is driven and/or regulated by that promoter. A person skilled in the art will understand that being operably linked to a promoter preferably means that the promoter is positioned upstream (i.e. at the 5'-end) of the operably linked nucleic acid. The distance to the operably linked nucleic acid may be variable, as long as the promoter of the present invention is capable of driving and/or regulating the transcription of the operably linked nucleic acid. For example, between the promoter and the operably linked nucleic acid, there might be a cloning site, an adaptor, a transcription or translation enhancer.

The operably linked nucleic acid may be any coding or non-coding nucleic acid. The operably linked nucleic acid may be in the sense or in the anti-sense direction. Typically in the case of genetic engineering of host cells, the operably linked nucleic acid is to be introduced into the host cell and is intended to change the phenotype of the host cell. Alternatively, the operably linked nucleic acid is an endogenous nucleic acid from the host cell.

The term "heterologous" as used herein is intended to be "heterologous to the promoter of the present invention". A nucleic acid that is heterologous to the promoter of the present invention is not naturally occurring in the nucleic acid sequences flanking the promoter of the present invention when it is in its biological genomic environment. While the nucleic acid may be heterologous to the promoter of the present invention, it may be homologous or native or heterologous or foreign to the plant host cell. The heterologous operably linked nucleic acid may be any nucleic acid (for example encoding any protein), provided that it comprises or it is flanked by at least one nucleotide which is normally not flanking the promoter of the present invention.

The term "transcription terminator" as used in (c) refers to a DNA sequence at the end of a transcriptional unit which signals termination of transcription. Terminators are 3'-non-translated DNA sequences usually containing a polyadenylation signal, which facilitates the addition of polyadenylate sequences to the 3'-end of a primary transcript. Terminators active in and/or isolated from viruses, yeasts, moulds, bacteria, insects, birds, mammals and plants are known and have been described in literature. Examples of terminators suitable for use in the genetic constructs of the present invention include the *Agrobacterium tumefaciens* nopaline synthase (NOS) gene terminator, the *Agrobacterium tumefaciens* octopine synthase (OCS) gene terminator sequence, the Cauliflower mosaic virus (CaMV) 35S gene terminator sequence, the *Oryza sativa* ADP-glucose pyrophosphorylase terminator sequence (t3'Bt2), the *Zea mays* zein gene terminator sequence, the rbcs-1A gene terminator, and the rbcs-3A gene terminator sequences, amongst others.

The present invention also provides an expression cassette, a transformation vector or a plant expression vector comprising a genetic construct as described above.

An "expression cassette" as meant herein refers to a minimal genetic construct necessary for expression of a nucleic acid. A typical expression cassette comprises a promoter-gene-terminator combination. An expression cassette may additionally comprise cloning sites, for example Gateway™ recombination sites or restriction enzyme recognition sites, to allow easy cloning of the operably linked nucleic acid or to allow the easy transfer of the expression cassette into a vector. An expression cassette may further comprise 5' untranslated regions, 3' untranslated regions, a selectable marker, transcription enhancers or translation enhancers.

With "transformation vector" is meant a genetic construct, which may be introduced in an organism by transformation and may be stably maintained in said organism. Some vectors may be maintened in for example *Escherichia coli, A. tumefaciens, Saccharomyces cerevisiae* or *Schizosaccharomyces pombe*, while others such as phagemids and cosmid vectors, may be maintained in bacteria and/or viruses. Transformation vectors may be multiplied in their host cell and may be isolated again therefrom to be transformed into another host cell. Vector sequences generally comprise a set of unique sites recognized by restriction enzymes, the multiple cloning site (MCS), wherein one or more non-vector sequence(s) can be inserted. Vector sequences may further comprise an origin of replication which is required for maintenance and/or replication in a specific host cell. Examples of origins of replication include, but are not limited to, the f1-ori and colE1.

"Expression vectors" form a subset of transformation vectors, which, by virtue of comprising the appropriate regulatory sequences, enable expression of the inserted non-vector sequence(s). Expression vectors have been described which are suitable for expression in bacteria (e.g. *E. coli*), fungi (e.g. *S. cerevisiae, S. pombe, Pichia pastoris*), insect cells (e.g. baculoviral expression vectors), animal cells (e.g. COS or CHO cells) and plant cells. One suitable expression vector according to the present invention is a plant expression vector, useful for the transformation of plant cells, the stable integration in the plant genome, the maintenance in the plant cell and the expression of the non-vector sequences in the plant cell.

Typically, a plant expression vector according to the present invention comprises a nucleic acid of any one of SEQ ID NO 1 to 22 or a variant thereof as described hereinabove, optionally operably linked to a second nucleic acid. Typically, a plant expressible vector according to the present invention, further comprises T-DNA regions for stable integration into the plant genome (for example the left border and the right border regions of the Ti plasmid).

The genetic constructs of the invention may further comprise a "selectable marker". As used herein, the term "selectable marker" includes any gene, which confers a phenotype to a cell in which it is expressed, to facilitate the identification and/or selection of cells that are transfected or transformed. Suitable markers may be selected from markers that confer antibiotic or herbicide resistance. Cells containing the genetic construct will thus survive antibiotics or herbicide concentrations that kill untransformed cells. Examples of selectable marker genes include genes conferring resistance to antibiotics (such as nptII encoding neomycin phosphotransferase capable of phosphorylating neomycin and kanamycin, or hpt encoding hygromycin phosphotransferase capable of phosphorylating hygromycin), to herbicides (for example bar which provides resistance to Basta; aroA or gox providing resistance against glyphosate), or genes that provide a metabolic trait (such as manA that allows plants to use mannose as sole carbon source). Visual marker genes result in the formation of colour (for example beta-glucuronidase, GUS), luminescence (such as luciferase) or fluorescence (Green Fluorescent Protein, GFP, and derivatives thereof). Further examples of suitable selectable marker genes include the ampicillin resistance (Ampr), tetracycline resistance gene (Tcr), bacterial kanamycin resistance gene (Kanr), phosphinothricin resistance gene, and the chloramphenicol acetyltransferase (CAT) gene, amongst others.

Furthermore, the present invention encompasses a host cell comprising an isolated promoter, or a genetic construct, or an expression cassette, or a transformation vector or an expression vector according to the invention as described hereinabove. In particular embodiments of the invention, the host cell is selected from bacteria, algae, fungi, yeast, plants, insect or animal host cells.

In one particular embodiment, the invention provides a transgenic plant cell comprising an isolated promoter according to the invention, or an isolated nucleic acid, or a genetic construct, or an expression cassette, or a transformation vector or an expression vector according to the invention as described hereinabove. Preferably said plant cell is a dicot plant cell or a monocot plant cell, more preferably a cell of any of the plants as mentioned herein. Preferably, in the transgenic plant cell according to the invention, the promoter or the genetic construct of the invention is stably integrated into the genome of the plant cell.

The invention also provides a method for the production of a transgenic plant, comprising:

(a) Introducing into a plant cell an isolated promoter, for example any one of SEQ ID NO 1 to SEQ ID NO 22, or a variant or fragment thereof, or a genetic construct, or an expression cassette, or a transformation vector or an expression vector according to the present invention and as described hereinabove, and

(b) Cultivating said plant cell under conditions promoting plant growth.

"Introducing" the above mentioned isolated promoter, or genetic construct, or expression cassette, or transformation vector or expression vector, into a host cell (e.g. plant cell) is preferably achieved by transformation. The term "transformation" as used herein encompasses the transfer of an exogenous polynucleotide into a host cell, irrespective of the method used for transfer. In particular for plants, tissues capable of clonal propagation, whether by organogenesis or embryogenesis, are suitable to be transformed with a genetic construct of the present invention and a whole plant may be regenerated therefrom. The particular tissue chosen will vary depending on the clonal propagation systems available for, and best suited to, the particular plant species being transformed. Exemplary tissue targets include leaf disks, pollen, embryos, cotyledons, hypocotyls, megagametophytes, callus tissue, existing meristematic tissue (e.g., apical meristem, axillary buds, and root meristems), and induced meristem tissue (e.g., cotyledon meristem and hypocotyl meristem). The polynucleotide may be transiently or stably introduced into a plant cell and may be maintained non-integrated, for example, as a plasmid. Alternatively, it may be integrated into the plant genome.

Transformation of a plant species is now a fairly routine technique. Advantageously, any of several transformation methods may be used to introduce the nucleic acids of the invention into a suitable ancestor cell. Transformation methods include the use of liposomes, electroporation, chemicals that increase free DNA uptake, injection of the DNA directly into the plant, particle gun bombardment, transformation using viruses or pollen and microprojection. Methods may be

selected from the calcium/polyethylene glycol method for protoplasts (Krens, F. A. et al., 1882, Nature 296, 72-74; Negrutiu I. et al., June 1987, Plant Mol. Biol. 8, 363-373); electroporation of protoplasts (Shillito R. D. et al., 1985 Bio/Technol 3, 1099-1102); microinjection into plant material (Crossway A. et al., 1986, Mol. Gen. Genet. 202, 179-185); DNA or RNA-coated particle bombardment (Klein T. M. et al., 1987, Nature 327, 70) infection with (non-integrative) viruses and the like. A preferred transformation method for the production of transgenic plant cells according to the present invention, is an *Agrobacterium* mediated transformation method.

Transgenic rice plants comprising any one of the promoters of the present invention are preferably produced via *Agrobacterium*-mediated transformation using any of the well-known methods for rice transformation, such as the ones described in any of the following: published European patent application EP 1198985 A1, Aldemita and Hodges (Planta, 199, 612-617, 1996); Chan et al. (Plant Mol. Biol. 22 (3) 491-506, 1993); Hiei et al. (Plant J. 6 (2) 271-282, 1994); which disclosures are incorporated by reference herein as if fully set forth. In the case of corn transformation, the preferred method is as described in either Ishida et al. (Nat. Biotechnol. 1996 June; 14(6): 745-50) or Frame et al. (Plant Physiol. 2002 May; 129(1): 13-22), which disclosures are incorporated by reference herein as if fully set forth.

Generally after transformation, plant cells or cell groupings are selected for the presence of one or more markers which are encoded by plant-expressible genes co-transferred with the gene of interest (which could be under the control of any of the promoters of the present invention), following which the transformed material may be cultivated under conditions promoting plant growth.

The resulting transformed plant cell may then be used to regenerate a transformed plant in a manner known to persons skilled in the art. Accordingly, the method for the production of a transgenic plant as described hereinabove, may further comprise regenerating a plant from said plant cell of (a).

The present invention further provides a plant comprising a plant cell as described hereinabove. The plants may also be able to grow, or even reach maturity including for example fruit production, seed formation, seed ripening and seed setting.

Furthermore, progeny may be produced from these seeds, which progeny may be fertile. Alternatively or additionally, the transformed and regenerated plants may also produce progeny by non-sexual propagation such as cloning, grafting. The generated transformed plants may be propagated by a variety of means, such as by clonal propagation or classical breeding techniques. For example, a first generation (or T1) transformed plant may be selfed to give homozygous second generation (or T2) transformants, and the T2 plants further propagated through classical breeding techniques.

The generated transformed organisms may take a variety of forms. For example, they may be chimeras of transformed cells and non-transformed cells; clonal transformants (e.g., all cells transformed to contain the expression cassette); grafts of transformed and untransformed tissues (e.g., in plants, a transformed rootstock grafted to an untransformed scion).

Following DNA transfer and growth of the transformed cells, putatively transformed plant cells or plants may be evaluated, for instance using Southern analysis, for the presence of the gene of interest, copy number and/or genomic organization. Alternatively or additionally, expression levels or expression patterns of the newly introduced DNA may be undertaken using northern and/or Western analysis, both techniques being well known to persons having ordinary skill in the art.

The present invention clearly extends to plants obtainable by any of the methods according to the present invention, which plants comprise any of the isolated promoters or the constructs of the present invention. The present invention clearly extends to any plant parts and propagules of such plant. The present invention extends further to encompass the progeny of a primary transformed cell, tissue, organ or whole plant that has been produced by any of the aforementioned methods, the only requirement being that progeny exhibit the same genotypic and/or phenotypic characteristic(s) as those produced in the parent by the methods according to the invention. The invention also extends to harvestable parts of a plant, such as but not limited to seeds, leaves, fruits, flowers, stem cultures, stem, rhizomes, roots, tubers, bulbs and cotton fibers.

The term "plant" or "plants" as used herein encompasses whole plants, ancestors and progeny of plants and plant parts, including seeds, shoots, stems, roots (including tubers), and plant cells, tissues and organs. The term "plant" therefore also encompasses suspension cultures, embryos, meristematic regions, callus tissue, gametophytes, sporophytes, pollen, and microspores. Plants that are particularly useful in the methods of the invention include all plants which belong to the superfamily Viridiplantae, in particular monocotyledonous and dicotyledonous plants including a fodder or forage legume, ornamental plant, food crop, tree, or shrub selected from the list comprising *Acacia* spp., *Acer* spp., *Actinidia* spp., *Aesculus* spp., *Agathis australis, Albizia amara, Alsophila tricolor, Andropogon* spp., *Arachis* spp, *Areca catechu, Astelia fragrans, Astragalus cicer, Baikiaea plurijuga, Betula* spp., *Brassica* spp., *Bruguiera gymnorrhiza, Burkea africana, Butea frondosa, Cadaba farinosa, Calliandra* spp, *Camellia sinensis, Canna indica, Capsicum* spp., *Cassia* spp., *Centroema pubescens, Chaenomeles* spp., *Cinnamomum cassia, Coffea arabica, Colophospermum mopane, Coroniffia varia, Cotoneaster serotina, Crataegus* spp., *Cucumis* spp., *Cupressus* spp., *Cyathea dealbata, Cydonia oblonga, Cryptomeria japonica, Cymbopogon* spp., *Cynthea dealbata, Cydonia oblonga, Dalbergia monetaria, Davallia divaricata, Desmodium* spp., *Dicksonia squarosa, Diheteropogon amplectens, Dioclea* spp, *Dolichos* spp., *Dorycnium rectum, Echinochloa pyramidalis, Ehrartia* spp., *Eleusine coracana, Eragrestis* spp., *Erythrina* spp., *Eucalyptus* spp., *Euclea schimperi, Eulalia villosa, Fagopyrum* spp., *Feijoa sellowiana, Fragaria* spp., *Flemingia* spp, *Freycinetia banksii, Geranium thunbergii, Ginkgo biloba, Glycine javanica, Gliricidia* spp, *Gossypium hirsutum, Grevillea* spp., *Guibourtia coleosperma, Hedysarum* spp., *Hemarthia altissima, Heteropogon contortus, Hordeum vulgare, Hyparrhenia rufa, Hypericum erectum, Hyperthelia dissoluta, Indigo incarnata, Iris* spp., *Leptarrhena pyrolifolia, Lespediza* spp., *Lettuca* spp., *Leucaena leucocephala, Loudetia simplex, Lotonus bainesii, Lotus* spp., *Macrotyloma axillare, Malus* spp., *Manihot esculenta, Medicago sativa, Metasequoia glyptostroboides, Musa sapientum, Nicotianum* spp., *Onobrychis* spp., *Ornithopus* spp., *Oryza* spp., *Peltophorum africanum, Pennisetum* spp., *Persea gratissima, Petunia* spp., *Phaseolus* spp., *Phoenix canariensis, Phormium cookianum, Photinia* spp., *Picea glauca, Pinus* spp., *Pisum sativum, Podocarpus totara, Pogonarthria fleckii, Pogonarthria squarrosa, Populus* spp., *Prosopis cineraria, Pseudotsuga menziesii, Pterolobium stellatum, Pyrus communis, Quercus* spp., *Rhaphiolepsis umbellata, Rhopalostylis sapida, Rhus natalensis, Ribes grossularia, Ribes* spp., *Robinia pseudoa-*

cacia, Rosa spp., *Rubus* spp., *Salix* spp., *Schyzachyrium sanguineum, Sciadopitys verticillata, Sequoia sempervirens, Sequoiadendron giganteum, Sorghum bicolor, Spinacia* spp., *Sporobolus fimbriatus, Stiburus alopecuroides, Stylosanthos humilis, Tadehagi* spp, *Taxodium distichum, Themeda triandra, Trifolium* spp., *Triticum* spp., *Tsuga heterophylla, Vaccinium* spp., *Vicia* spp. *Vitis vinifera, Watsonia pyramidata, Zantedeschia aethiopica, Zea mays*, amaranth, artichoke, asparagus, broccoli, brussel sprout, cabbage, canola, carrot, cauliflower, celery, collard greens, flax, kale, lentil, oilseed rape, okra, onion, potato, rice, soybean, straw, sugarbeet, sugar cane, sunflower, tomato, squash, and tea, trees and algae amongst others. According to a preferred feature of the present invention, the plant is a crop plant such as soybean, sunflower, canola, alfalfa, rapeseed, cotton, tomato, potato, tobacco, squash, papaya, poplar, leguminosa, flax, lupinus or sorghum. According to another preferred embodiment of the present invention the plant is a monocotyledonous plant, such as sugarcane, further preferable a cereal such as rice, maize, wheat, barley, millet, rye or oats.

The invention further provides a method for driving and/or regulating expression of a nucleic acid in a plant or plant cell, comprising:

a) Operably linking a nucleic acid to an isolated nucleic acid according to the invention as described hereinabove, such as to any one of SEQ ID NO 1 to 22 or a variant or fragment thereof, and

b) Introducing the resultant genetic construct into a plant or plant cell.

Preferably the operably linked nucleic acid of (a) is heterologous to the nucleic acids according to the present invention.

This method may further comprise cultivating the transformed plant or plant cell under conditions promoting growth, promoting regeneration and/or promoting maturation.

Furthermore, the expression of the operably linked nucleic acid may be driven and/or regulated in particular cells, tissues or organs of a plant. Accordingly, the invention provides a method as described above, wherein the expression is constitutive expression or tissue-specific expression. For these embodiments, reference is made to the example section where the specific expression patterns of the promoters according to the invention are described and where different types of tissue-specific expression are detailed.

The present invention further encompasses the use of an isolated nucleic acid as defined hereinabove to drive and/or regulate expression of an operably linked nucleic acid.

(i) The person skilled in the art will recognize that provision of sequences SEQ ID NO 1 to 22, readily makes available the tools to isolate related promoters, which may have substantial sequence identity to any of SEQ ID NO 1 to 22. Additionally, provision of sequences SEQ ID NO 23 to 44 (CDS corresponding to the promoters of the present invention, see Table 1), readily makes available the tools to isolate related promoters, of which the related CDSs may have substantial sequence identity to any of SEQ ID NO 23 to 44. Therefore the present invention also encompasses a method for isolating nucleic acids, capable of driving and/or regulating expression of an operably linked nucleic acid, comprising screening a nucleic acid sequence database to find homologues of any of the sequences represented by SEQ ID NO 1 to 22 or SEQ ID NO 23 to 44. Subsequently these homologues are used to screen a library with genomic DNA, which library is for example prepared from the organism of origin of the above mentioned homologue. The screening procedure may for example involve hybridization. Subsequently, the genomic DNA that matches the homologue, is analysed to identify the transcription initiation site and the translation initiation site of the gene corresponding to the homologue. Finally, specific primers are designed for amplification of a nucleic acid located in the region upstream (at the 5' end) of said translation initiation site.

The present invention extends to the identification of regulatory proteins that are involved in the regulation of the activity of the promoters according to the present invention. Such identification may be achieved using a yeast one-hybrid system. In such a yeast one-hybrid system the sequences according to any one of SEQ ID NO 1 to 22 are operably linked to the GAL transcription activator and transformed to a yeast cell culture. That yeast cell culture is again transformed with a library of constructs encoding candidate regulatory factors.

The present invention will now be described with reference to the following figures in which:

FIG. **1** shows a general schematic representation of a promoter. Regulatory elements are sequences that may for example be responsible for special and/or temporal regulation of the promoter activity. The minimal promoter is the minimal sequence necessary and sufficient to drive expression. It includes a TATA box, which is necessary to correctly direct the RNA polymerase II to the transcription initiation site. The transcription initiation element (INR) includes the transcription initiation start site. The 5' untranslated region (5'UTR) is the region that is transcribed into pre-messenger RNA and eventually into mRNA, but is not translated into protein. The translation initiation codon is represented by the startcodon ATG.

FIG. **2** is a map of the vector p4581 useful for expression in plants of a β-glucuronidase (GUS) gene under control of any one of the promoters according to the invention. This binary vector comprises a Gateway recombination cassette, suitable for the recombination cloning of any of the promoters of the present invention in front of the *Escherichia coli* β-glucuronidase (GUS) gene. This cassette contains a chloramphenicol resistance gene (CamR) and the ccdB suicide gene for counter selection of non-recombined plasmids, This GUS expression cassette further comprises the double terminator sequence T-zein and T-rbcS-deltaGA. This expression cassette is located within the left border (LB repeat, LB Ti C58) and the right border (RB repeat, RB Ti C58) of the nopaline Ti plasmid. Cloned within these borders are also selectable marker and a screenable marker genes each under control of a constitutive promoter and a terminator sequence. This vector also contains an origin of replication (pBR322) for bacterial replication and a bacterial selectable marker (Spe/SmeR) for bacterial selection.

The following figures show the results of the GUS staining of plants or plant parts transformed with the reporter vector p4581 carrying a promoter according to the present invention operably linked to the reporter gene GUS. Plants denoted "C plants" are transgenic plants grown to about 5 cm; Plants denoted "B plants" are grown to about 10 cm; and plants denoted "A plants" are grown to maturity. These A plants were used to collect different tissue samples from old leaves, young leaves and seeds.

FIG. **3** shows the expression pattern of PRO0110 (RCc3, SEQ ID NO 1). GUS staining is visible in roots.

FIG. **4** shows the expression pattern of PRO0005 (putative beta-amylase, SEQ ID NO 2). GUS staining is visible in seeds, more specifically in the embryo or in the scutellum of the embryo.

FIG. **5** shows the expression pattern of PRO0009 (putative cellulose synthetase, SEQ ID NO 3). GUS staining is visible in roots.

FIG. **6** shows the expression pattern of PRO0058 (proteinase inhibitor Rgpi9, SEQ ID NO 4). GUS staining is visible in the seeds.

FIG. **7** shows the expression pattern of PRO0061 (beta expansine EXPB9, SEQ ID NO 5). GUS staining is visible in young flowers of A plants (A) and in other young expanding tissues of B plants (B) and C plants (C).

FIG. **8** shows the expression pattern of PRO0063 (putative structural protein, SEQ ID NO 6). GUS staining is visible in young tissues, for example in the calli (A) or old leaves, young leaves and seeds of "A plants" (B).

FIG. **9** shows the expression pattern of PRO0081 (putative caffeoyl-CoA 3-O-methyltransferase, SEQ ID NO 7). GUS staining is visible in young tissues, particularly of the shoot.

FIG. **10** shows the expression pattern of PRO0091 (prolamine RP5, SEQ ID NO 8). GUS staining is visible in seeds (A), particularly in the endosperm, and in meristem (B).

FIG. **11** shows the expression pattern of PRO0095 (putative amino peptidase, SEQ ID NO 9). GUS staining is visible in seeds, more particularly in the embryo.

FIG. **12** shows the expression pattern of PRO0111 (uclacyanin 3-like protein, SEQ ID NO 10). GUS staining is visible in roots and in meristem.

FIG. **13** shows the expression pattern of PRO0116 (26S proteasome regulatory particle non-ATPase subunit 11, SEQ ID NO 11). GUS staining is weakly visible in the whole plant (weak constitutive) and is particularly visible in meristem.

FIG. **14** shows the expression pattern of PRO0117 (putative 40S ribosomal protein, SEQ ID NO 12). GUS staining is visible in the seeds, more particularly in the endosperm.

FIG. **15** shows the expression pattern of PRO0122 (chlorophyll a/b-binding protein presursor (Cab27), SEQ ID NO 13). GUS staining is visible in the shoot.

FIG. **16** shows the expression pattern of PRO0123 (putative protochlorophyllide reductase, SEQ ID NO 14). GUS staining is visible in the shoot (above-ground tissues).

FIG. **17** shows the expression pattern of PRO0133 (chitinase Cht-3, SEQ ID NO 15). GUS staining is visible in the roots and meristem.

FIG. **18** shows the expression pattern of PRO0151 (WSI18, SEQ ID NO 16). GUS staining is visible in the calli and upper plant parts (A) as well as in the aleurone layer and embryo (B).

FIG. **19** shows the expression pattern of PRO0169 (aquaporine, SEQ ID NO 17). GUS staining is visible in the whole plant (constitutive expression).

FIG. **20** shows the expression pattern of PRO0170 (High mobility group protein, SEQ ID NO 18). GUS staining is strongly visible in the whole plant as is illustrated by the "B plants" (A), and various tissues such as old leaves, young leaves and seeds (B) and calli (C) (constitutive expression).

FIG. **21** shows the expression pattern of PRO0171 (reversibly glycosylated protein RGP1, SEQ ID NO 19). GUS staining is visible in all plant parts (constitutive expression).

FIG. **22** shows the expression pattern of PRO0173 (cytosolic MDH, SEQ ID NO 20). GUS staining is visible in all plant parts and particularly in the shoot (above-ground tissues) and seeds.

FIG. **23** shows the expression pattern of PRO0175 (RAB21, SEQ ID NO 21). GUS staining is weakly visible in calli (A), meristems and young leaves, and is strongly visible in developing and maturing seeds (B) more particularly in the embryo.

FIG. **24** shows the expression pattern of PRO0177 (Cdc2-1, SEQ ID NO 22). GUS staining is weakly visible in meristem and in leaf sheets.

EXAMPLES

The promoters according to the present invention were isolated as DNA regions spanning about 1.2 kb of the sequence upstream of the translation initiation codon (i.e. first ATG, which codon was excluded) from various rice genes. For determination of their nucleic acid sequence and their expression pattern, the following procedure was followed: First in silico studies on genomic rice sequences were performed. However, procedures based on automated prediction programs to locate promoter-like nucleic acid sequence are highly error prone, even for the localization the best-characterized promoter control elements such as the TATA box and the transcription initiation element (INR). Also, in silico determination of expression pattern is extremely speculative. Therefore, to obtain unambiguous data about the nucleic acid sequence and the expression pattern of the promoters, in vivo studies were performed encompassing (i) isolation of the promoter nucleic acid sequence; (ii) operably linking a reporter gene to the promoter and introducing the resulting genetic construct into a host organisms; (iii) growing the transformed host cell under conditions allowing expression of the reporter gene, and (iv) determination of the reporter gene activity in the different tissues of the host organism. These methods are now described in more detail.

Example 1

Identification and Isolation of the Promoters

Identification of Rice ESTs, the Corresponding Genes and their Location in the Rice Genome

Sequence databases, comprising rice sequences, were searched for rice expressed sequence tags (ESTs). Subsequently an "in silico" Northern-blot was performed to allow identification of EST families that are strongly expressed or that are specific for a particular organ. This analysis included normalization of the numbers of ESTs isolated from different plant organs. The ESTs families with an interesting distribution among source cDNA libraries were selected for further analysis and sequence homology searches. After sequence homology searches in combination with scanning scientific data, the genes that correspond to those families of ESTs were identified from sequence databases and a (putative) function and corresponding gene name was given (see Table 1). Subsequently, the corresponding promoter region was isolated by the following procedure. In a first step the TIGR database was searched to find a tentative contig corresponding to an EST family. Sequence homology was found using standard computer programs, such as Blast N using standard parameters (typically G Cost to open a gap=5, E Cost to extend a gap=2, q Penalty for a mismatch in the blast portion of run=−3, r Reward for a match in the blast portion of run=1, e Expectation value=10.0, W Word size=11, v Number of one-line descriptions=100, b Number of alignments to show=100, Matrix=BLOSUM62). The TIGR database (The Institute for Genomic Research), provides Tentative Contigs (TC) which are sequence predictions based on contig building from all known EST, from all known cDNA and from reconstructed mRNA. The TCs used for identification of the promoters of the present invention are represented in Table 1. In a second step these TCs were used to locate the corresponding gene on a genomic sequence, which gene comprises the coding region as well as the promoter region. Generally, these genomic sequences were BAC clones, which are represented herein by their Genbank accession number (see Table 1). From these BAC clones the sequence identity of the promoter region could be determined.

TABLE 1

list of rice promoters of the present invention. The promoter sequences are represented herein by their SEQ ID NO and promoter number (PRO). The coding sequences (CDS) naturally driven by a promoter of the present invention are represented by their name, by SEQ ID NO and by Tentative contig (TC) accession number of the TIGR database. The Genomic sequences (BAC clones or genes) comprising a promoter region of the present invention are represented by their Genbank accession number.

Prom SEQ ID NO	Prom number	CDS name	CDS SEQ ID NO	CDS TC	BAC clone (*or gene)
1	PRO0110	RCc3	23	TC89946	AC037426
2	PRO0005	putative beta-amylase	24	TC90358	AC022457
3	PRO0009	putative cellulose synthase	25	TC83635	AC022457
4	PRO0058	proteinase inhibitor Rgpi9	26	TC83117	AF044059
5	PRO0061	beta expansine EXPB9	27	TC89913	AC020666
6	PRO0063	structural protein	28	TC89985	AP001278
7	PRO0081	putative caffeoyl-CoA 3-O-methyltransferase	29	TC89891	AP000364
8	PRO0091	prolamine RP5	30	TC89670	AF156714*
9	PRO0095	putative methionine aminopeptidase	31	TC89883	AC027133
10	PRO0111	uclacyanin 3-like protein	32	TC90434	AJ307662
11	PRO0116	26S proteasome regulatory particle non-ATPase subunit 11	33	TC83072	AP000969
12	PRO0117	putative 40S ribosomal protein	34	TC90038	AC090871
13	PRO0122	chlorophyll a/b-binding protein presursor (Cab27)	35	TC82936	AP004700
14	PRO0123	putative protochlorophyllide reductase	36	TC89839	AL606456
15	PRO0133	chitinase Cht-3	37	TC85888	D16223*
16	PRO0151	WSI18	38	TC84300	AP003023
17	PRO0169	aquaporine	39	TC89687	AP005108
18	PRO0170	High mobility group protein	40	TC89846	AP004004
19	PRO0171	reversibly glycosylated protein RGP1	41	TC82935	AC090874
20	PRO0173	cytosolic MDH	42	TC82977	AC037425
21	PRO0175	RAB21	43	TC83646	Y00842*
22	PRO0177	Cdc2-1	44	TC90619	AP004765

Identification and Isolation of the Promoter Regions of Rice Genes

Starting from the sequence information of the genes and their location in the rice genome, the promoter regions of these genes were isolated as the DNA region spanning about 1.2 kb upstream of the translation initiation codon (i.e. first ATG), which codon was excluded. When an intervening sequence such as an intron, was present in the 5' untranslated region of the gene, the isolated DNA region was taken as the region spanning about 1.2 kb plus the length of that intervening sequence. The promoter regions were isolated from genomic DNA of *Oryza sativa Japonica* or exceptionally from *Oryza sativa Indica* via PCR using specific primers. These specific primers comprise AttB recombination sites, suitable for recombination cloning of the isolated promoter region These specific primers are herein represented as SEQ ID NO 45 to 88 and are listed in Table 2. Conditions for PCR were as follows: 1 cycle of 2 min at 94° C., 35 cycles of 1 min at 94° C., 1 min at 58° C. and 2 min at 68° C., and 1 cycle of 5 min at 68° C. The length of the expected PCR fragment is also indicated in Table 2. The corresponding PCR fragment was purified from the PCR reaction mix via gele electrophoresis and subsequent purification using Zymoclean Gel DNA Recovery Kit (Zymo Research, Orange, Calif.).

TABLE 2

Overview of the primers used to isolate the rice promoters of the present invention and the length of the rice promoter regions.

Promoter SEQ ID NO	Promoter number	Prom length	Primer forward SEQ ID NO	Primer forward	Primer reverse SEQ ID NO	Primer reverse
1	PRO0110	1264	45	prm3780	67	prm3781
2	PRO0005	1215	46	prm2768	68	prm2769

TABLE 2-continued

Overview of the primers used to isolate the rice promoters of the present invention and the length of the rice promoter regions.

Promoter SEQ ID NO	Promoter number	Prom length	Primer forward SEQ ID NO	Primer forward	Primer reverse SEQ ID NO	Primer reverse
3	PRO0009	1038	47	prm2420	69	prm2421
4	PRO0058	1301	48	prm2853	70	prm2854
5	PRO0061	1243	49	prm2426	71	prm2427
6	PRO0063	1019	50	prm2855	72	prm2856
7	PRO0081	1212	51	prm3025	73	prm3026
8	PRO0091	1052	52	prm3029	74	prm3030
9	PRO0095	1216	53	prm3061	75	prm3062
10	PRO0111	1237	54	prm3031	76	prm3032
11	PRO0116	1100	55	prm3051	77	prm3052
12	PRO0117	1216	56	prm3592	78	prm3049
13	PRO0122	1210	57	prm5131	79	prm2195
14	PRO0123	123	58	prm3782	80	prm2197
15	PRO0133	1808	59	prm2844	81	prm2845
16	PRO0151	1828	60	prm2973	82	prm2974
17	PRO0169	1267	61	prm3770	83	prm3771
18	PRO0170	1130	62	prm3772	84	prm3773
19	PRO0171	1230	63	prm3774	85	prm3775
20	PRO0173	1234	64	prm3776	86	prm3777
21	PRO0175	1553	65	prm3800	87	prm3801
22	PRO0177	1087	66	prm5135	88	prm5136

Example 2

Cloning of Promoter-GUS Reporter Vectors for Plant Transformation

The purified PCR fragments of Example 1, corresponding to the promoter regions of the present invention, were cloned into the pDONR201 entry plasmid of the Gateway™ system (Life Technologies) using the "BP recombination reaction".

The identity and base pair composition of the cloned insert was confirmed by sequencing and additionally, the resulting plasmid was tested via restriction digests.

In order to clone each of the promoters of the present invention in front of a reporter gene, each entry clone of Example 1 was subsequently used in an "LR recombination reaction" (Gateway TM) with the destination vector p4581. This destination vector was designed to operably link each promoter of the present invention to the *Escherichia coli* beta-glucuronidase (GUS) gene via the substitution of the Gateway recombination cassette in front of the GUS gene. Furthermore this destination vector is suitable for transformation of plants and comprises within the T-DNA left and right borders the resulting promoter-GUS cassette and selectable marker and screenable marker cassettes (see FIG. **2**). The resulting reporter vectors, comprising a promoter of the present invention operably linked to GUS, are subsequently transformed into *Agrobacterium* strain LBA4044 and subsequently into rice plants using standard transformation techniques.

Example 3

Expression Patterns of the Promoter-GUS Reporter Cassette in Plants

Growth and Harvest of Transgenic Plants or Plant Parts at Various Stages (C Plants, B Plants and A Plants)

For each promoter-GUS reporter construct, 3 T0 transgenic rice plants were generated from transformed cells. Plant growth was performed under normal conditions. The first transgenic plant was sacrificed for GUS staining when it had reached a size of about 5 cm, which plant is named herein "C plant". The second transgenic plant was sacrificed for GUS staining when it had reached a size of about 10 cm, which plant is named herein "B plant". The third transgenic plant was kept for seed production and is named herein "A plant". GUS staining was performed on complete C and B plants. On A plants, GUS staining was performed on leaf pieces, flowers and section of seeds at various developmental stages. A plants were allowed to set seed, which seeds were used after harvest for confirmation of the expression pattern in T1 plants.

GUS Staining

The sacrificed plants or plant parts were covered with 90% ice-cold acetone and incubated for 30 min at 4° C. After 3 washes of 5 min with Tris buffer [15.76 g Trizma HCl (Sigma T3253)+2,922 g NaCl in 1 I bidi, adjusted to pH 7.0 with NaOH], the material was covered by a Tris/ferricyanate/X-Gluc solution [9.8 ml Tris buffer+0.2 ml ferricyanate stock (0.33 g Potassium ferricyanate (Sigma P3667) in 10 ml Tris buffer)+0.2 ml X-Gluc stock (26.1 mg X-Gluc (Europa Bioproducts ML 113A) in 500 µl DMSO)]. Vacuum infiltration was applied for 15 to 30 minutes. The plants or plant parts were incubated for up to 16 hours at 37° C. until development of blue colour was visible. The samples were washed 3 times for 5 minutes with Tris buffer. Chlorophyll was extracted in ethanol series of 50%, 70% and 90% (each for 30 minutes).

Expression Patterns of the Promoters of the Present Invention

The expression patterns of the rice promoters of the present invention are summarized in Table 3.

TABLE 3

expression patterns of the rice promoters of the present invention

PRO SEQ ID NO	Promoter number	Promoter name	Expression pattern
1	PRO0110	RCc3	strong root
2	PRO0005	putative beta-amylase	Embryo (scutellum)
3	PRO0009	putative cellulose synthase	weak in roots
4	PRO0058	proteinase inhibitor Rgpi9	seed
5	PRO0061	beta expansine EXPB9	weak in young tissues
6	PRO0063	structural protein	young tissues + calli + embryo
7	PRO0081	putative caffeoyl-CoA 3-O-methyltransferase	shoot
8	PRO0091	prolamine RP5	meristem + strong in endosperm
9	PRO0095	putative methionine aminopeptidase	embryo
10	PRO0111	uclacyanin 3-like protein	weak meristem
11	PRO0116	26S proteasome reg. particle non-ATPase s.u. 11	weak meristem
12	PRO0117	putative 40S ribosomal protein	weak in endosperm
13	PRO0122	chlorophyll a/b-binding protein presursor (Cab27)	weak in shoot
14	PRO0123	putative protochlorophyllide reductase	strong shoot specific
15	PRO0133	chitinase Cht-3	weak meristem specific
16	PRO0151	WSI18	Calli + shoot + strong embryo
17	PRO0169	aquaporine	medium constitutive
18	PRO0170	High mobility group protein	strong constitutive
19	PRO0171	reversibly glycosylated protein RGP1	weak constitutive
20	PRO0173	cytosolic MDH	Shoot and seed
21	PRO0175	RAB21	embryo
22	PRO0177	Cdc2-1	weak in meristem + strong seed

The following paragraphs describe the observed expression patterns of the promoters of the present invention in more detail. The observations are based on the visual inspection of the GUS stained tissues as described above. It is to be understood that for some promoters expression may be weak and that expression in certain tissues may only be visible with very sensitive detection methods.

PRO0110—SEQ ID NO 1-RCc3

1 construct (OS1432), which is a reporter vector as described in Example 2 comprising PRO0110 was investigated. 25 calli, 14 C, 21 B plants and 21 A plants were analysed. There was no expression visible in calli, but strong expression in roots of C plants (93%) and of B plants (81%) was observed. No expression in the shoots of A plants was observed. Therefore the RCc3 promoter PRO0110 is suitable for strong expression in roots.

PRO0005—SEQ ID NO 2—Putative Beta-Amylase

1 construct (OS1365) was investigated. 28 calli, 24 B plants and 22 A plants were analysed. Occasional expression in calli (7%) was observed as well as occasional weak expression in roots (4%) and shoots (12%) of B plants, expression in the scutellum of embryos of A plants (43%) and occasional expression in leaves (5%) of A plants. This promoter is therefore suitable for expression in embryo, more preferably in the scutellum of the embryo. This region of the embryo is also referred to as the transfer layer of the embryo. This promoter may have some leakiness in other tissues.

PRO0009—SEQ ID NO 3—Putative Cellulose Synthase

1 construct (OS1461) was investigated. 20 calli, 20 C, 20 B plants and 20 A plants were analysed. Occasional expression in calli (20%) was observed as well as weak expression in roots (55%) of C plants, occasional expression in young leaves (10%) of C plants and weak expression in the roots (25%) of B plants. No expression in leaves of A or B plants was observed. Therefore this promoter is suitable for expression in roots. This promoter may show some leakiness in the leaves.

PRO0058—SEQ ID NO 4—Proteinase Inhibitor Rgpi9

1 construct (OS1370) was investigated. 13 B plants and 12 A plants were analysed. No expression was observed in B plants. In A plants, no expression was observed in the leaves, but there was strong expression in endosperm and embryo (58-42%). Therefore, this promoter PRO0058 is suitable for expression in seeds.

PRO0061—SEQ ID NO 5—Beta Expansine EXPB9

2 constructs (OS1441 and OS1460) were investigated. 20 calli, 32 C, 32 B plants and 32 A plants were analysed. Weak expression was observed in the leaves of C and B plants. In A plants expression in the flowers was observed (44%), more particularly in lemma of young spikelets. It was concluded that the promoter PRO0061 is suitable for expression in young tissue, more preferably in young, developing or expanding tissue, more preferably in green tissue.

PRO0063—SEQ ID NO 6—Putative Structural Protein

1 construct (OS1446) was investigated. 13 calli, 13 C, 13 B plants and 12 A plants were analysed. In calli, weak expression was detected (92%). In C plants, there was no expression in roots and there was weak expression in some leaves (46%). In B plants, there was no expression in roots and weak expression in young tillers (78%) or young leaves (54%), but no expression in old leaves. In A plants, there was occasional expression in young leaves (17%) and expression in embryo and scutellum (42%). Therefore it was concluded that this promoter is active in the above-ground tissues, such as leaf, stem and seed. These data demonstrate that the promoter is suitable for expression in calli and in the shoot, and for expression in young tissues and seeds.

PRO0081—SEQ ID NO 7—Putative Caffeoyl-CoA 3-O-methyltransferase

1 construct (OS1419) was investigated. 20 calli, 20 C, 20 B plants and 20 A plants were analysed. No expression was observed in Calli. Expression was observed in C plants, more particularly weak expression in root cylinder (40%) and weak expression in young leaves (80%) and in old leaves. Expression was also observed in B plants, more particularly weak expression in roots (25%) and weak expression in young leaves (80%). Expression was also observed in young leaves (50%) of A plants. It was concluded that promoter PRO0081 is suitable for expression in above-ground tissues, preferably in the shoot. This promoter may have some leakage of expression in roots.

PRO0091—SEQ ID NO 8—Prolamine RP5

1 construct (OS1558) was investigated. 12 C, 12 B plants and 12 A plants were analysed. Weak expression was observed in the discrimination centre (50%) of C plants and in the discrimination centre (58%) of B plants. Strong expression was observed in endosperm (55%) of A plants. This promoter was found to be useful for strong expression in the endosperm, with leakiness in meristem, preferably the shoot meristem or discrimination centre.

PRO0095—SEQ ID NO 9—Putative Methionine Aminopeptidase

1 construct (OS1423) was investigated. 16 calli, 14 C, 14 B plants and 16 A plants were analysed. Some expression was observed in root-tips (36%) of C plants and in the embryo (38%) of A plants, but not in endosperm of A plants. It was concluded that PRO0095 is suitable for expression in embryo.

PRO0111—SEQ ID NO 10—Uclacyanin 3-Like Protein

1 construct (OS1421) was investigated. 22 calli, 21 C, 22 B plants and 21 A plants were analysed. Weak expression was observed in the discrimination centre and meristems (77%) of B plants. It was concluded that promoter PRO0111 is suitable for weak expression in the meristem, preferably in shoot meristem or discrimination centre.

PRO0116—SEQ ID NO 11-26S Proteasome Regulatory Particle Non-A TPase Subunit 11

1 construct (OS1679) was investigated. 13 C, 14 B plants and A plants were analysed. Weak expression was observed in meristem/discrimination centre of C plants (38%) and of B plants (71%) and in young leaf sheaths of C plants (77%) and of B plants (21%). It was concluded that promoter PRO0116 is suitable for expression in meristem, preferably in shoot meristem or discrimination centre.

PRO0117—SEQ ID NO 12—Putative 40S Ribosomal Protein

1 construct (OS1425) was investigated. 9 calli, 9 C, 9 B plants and 9 A plants were analysed. Occasional weak expression was observed in roots (22%) and in young leaf blades (44%) of C plants. Expression was mainly observed in endosperm (37%) of A plants. Therefore, promoter PRO117 was found to be suitable for expression in endosperm and may have some leakiness in young leaves.

PRO0122—SEQ ID NO 13—Chlorophyll a/b-Binding Protein Presursor (Cab27)

1 construct (OS1675) was investigated. 38 calli, 38 C, 38 B plants and 15 A plants were analysed. Very weak expression was observed in the discrimination centre and young leaf sheaths of C plants. It was concluded that this promoter PRO0122 is suitable for weak expression in shoots.

PRO0123—SEQ ID NO 14—Putative Protochlorophyllide Reductase

1 construct (OS1433) was investigated. 21 calli, 18 C, 19 B plants and 18 A plants were analysed. Strong expression was observed in shoots (33-68%) of C plants and B plants (63-

79%). In B plants there was also occasional expression in roots. In A plants, again strong expression in young leaves (73%) was observed, as well as occasional expression in old leaves (39%). It was concluded that this promoter is suitable for strong expression in shoots, preferably in leaves.

PRO0133—SEQ ID NO 15—chitinase Cht-3

1 construct (OS1687) was investigated. 15 calli, 12 C, 16 B plants and 12 A plants were analysed. Weak expression was observed in calli (66%) and in the discrimination centre/meristem (50%) of B plants. It was concluded that promoter PRO0133 is suitable for weak expression in meristem, preferably in shoot meristem or discrimination centre.

PRO0151—SEQ ID NO 16—WSI18

1 construct (OS1458) was investigated. 22 calli, 16 C, 16 B plants and 13 A plants were analysed. Strong expression was observed in calli (91%) and weak expression in shoots of C plants (62%). In A plants there was very strong expression in the aleurone layer and in the embryo (46%). It was concluded that promoter PRO0151 is suitable for strong expression in calli and in seeds, more particularly in the aleurone layer and in the embryo of the seeds.

PRO0169—SEQ ID NO 17—Aquaporine

1 construct (OS1911) was investigated. 11 calli, 10 C plants, B plants and A plants were analysed. Some expression (55%) was observed in calli and in roots (30%) of C plants. Furthermore, good expression was observed in shoot tissues (80%) of C plants and in young leaves of B plants. It was concluded that this promoter is suitable for constitutive expression, preferably constitutive in young plants.

PRO170—SEQ ID NO 18—HIGH MOBILITY GROUP PROTEIN

1 construct (OS1434) was investigated. 23 calli, 21 C, 21 B plants and 14 A plants were analysed. Expression was observed in calli (52%) and in roots (51%) of C plants. Moreover, strong expression was observed in young leaves (81%) of C plants, in roots (86%) of B plants and in young leaves (86%) of B plants. In A plants there was strong expression in young leaves (75%), old leaves (43%), embryo and aleurone but a weaker expression in endosperm (82%). It was concluded that promoter PRO170 is suitable for strong constitutive expression.

PRO0171—SEQ ID NO 19—Reversibly Glycosylated Protein RGP1

1 construct (OS1762) was investigated. 18 calli, 11 C and 13 B plants were analysed. Strong expression was observed in calli (44%) and in all tissues (27%) of C plants. In all tissues of B plants (16%), expression was somewhat weaker but most pronounced the in discrimination centres (46%). It was concluded that promoter PRO0171 is suitable for constitutive expression.

PRO0173—SEQ ID NO 20—Cytosolic MDH

1 construct (OS1435) was investigated. 17 calli, 17 C, 17 B plants and 15 A plants were analysed. Occasional expression (12%) was observed in calli and weak expression was observed in upper parts (24-69%) of C plants as well as in young leaves (41%) of B plants. In A plants, expression in leaves (33%) was observed and strong expression in seeds (38%), but not in the root. It was concluded that the promoter PRO0173 is suitable for expression in above-ground tissues especially for constitutive expression in the shoot and especially in the seeds.

PRO0175—SEQ ID NO 21—RAB21

1 construct (OS1436) was investigated. 16 calli, 12 C, 15 B plants and 15 A plants were analysed. Expression was observed in some calli (31%), in the discrimination centres (42%) of C plants and in young leaves (25-58%) of C plants and A plants (15%). Furthermore, very strong expression was observed in aleurone and embryo (60%) of a plant. It was concluded that promoter PRO0175 is suitable for strong expression in calli and in seeds, more particularly in developing/maturing seeds, more particularly in the aleurone layer and in the embryo of the seeds.

PRO0177—SEQ ID NO 22-Cdc2-1

1 construct (OS1436) was investigated. 16 calli, 12 C, 15 B plants and 15 A plants were analysed. Expression was observed in some of the calli (31%), in the discrimination centre (42%) of C plants, in young leaves (25-58%) of C plants and occasionally in young leaves (15%) of A plants. Moreover, very strong expression was observed in aleurone and embryo (60%) of seeds from A plants. It was concluded that this promoter is suitable for specific expression in seeds, more particularly in developing/maturing seeds.

Example 4

Stability of the Expression Patterns of the Promoters of the Present Invention in Further Generations

The above-mentioned analyses were performed on T0 plants originating from the transformed tissues. The stability of promoter activity in the next generations or progeny plants of the original T0 plant, the so-called T1 and T2 plants, was evaluated as follows. The T0 plant transformed with the reporter constructs as mentioned in the above paragraphs of Example 2, were grown until maturity (A plants), of which the seeds (T1 seeds) were harvested and sown to generate progeny T1 plants. These plants were analysed as described above in Example 3 and the A T1 plants were allowed to reach maturity and to set T2 seeds.

The expression pattern of the promoters of the present invention was studied in T0 plants, T1 seeds, T1 plants and T2 seeds and in all the tissues (including seeds and seed tissues) as described in Example 3. The specific expression patterns as reported from the T0 and T1 seeds and described in Example 3 were confirmed in the following T1 generation and T2 seeds. It is concluded that the expression pattern of the promoters of the present are stably inherited in plants of subsequent generations.

Example 5

Stability of Expression Patterns of the Promoters of the Present Invention in Other Plants

The above-mentioned plant analyses were performed on rice plants. This choice was based on the practical consideration that plant genetic engineering is most profitable for crop plants. Also in other crop plants, such as for example *Zea Mays*, the reporter constructs comprising the promoters according to the present invention are introduced and transformed plant are evaluated as described hereinabove. The expression patterns of the promoters according to the present invention are conserved among plants. Therefore, the promoters according to the present invention are also suitable for driving and/or regulating expression of an operably linked nucleic acid in monocots, such as corn.

For many other purposes such as research and horticulture, (small) herbs are being genetically modified, which involves the use of promoters. Therefore the reporter constructs comprising the promoters according to the present invention are introduced into other plants species such as for example *Arabidopsis thaliana* and transformed plants are evaluated as described hereinabove. The expression patterns of the promoters according to the present invention are conserved among plants. Therefore, the promoters according to the present invention are also suitable for driving and/or regulating expression of an operably linked nucleic acid in other plant species such as for example dicots, such as *Arabidopsis*.

SEQUENCE LISTING

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<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: PRO0111 - uclacyanin 3-like protein

<400> SEQUENCE: 10

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tgatcaccct ccacaaagaa atggtacagt acatctccgt cccaaaataa gtgcagccat 120

gtatatccat gcctaacgtt tgaccgtccg tcttatttaa aaaaattatg aaaaatttaa 180

aaatatttag tcacacataa agtattattc atgttttatc atctaatagc aacaaaaaat 240

actaatcata aaatttttt taataagata aacggttaaa cgttgaacgt gaatagtgca 300

aaacttattt tagaacggag ggagtacgaa gtaactccgg aactacatat agggcaatta 360

ttgccctatg tatgcatata gtcaatcaat taactgctga caatggaaaa gctaatcaat 420

caatcaatgg tttgattaat caaattaagc caggtcagtc cgtcagtgta cattcactaa 480

ttaaattaac aggtttgttc aacggttcaa ccaacatctg ccatcaacat cttttcgttg 540

caccttttctt gactctttat gctattttgc taaaaaaaaa cttctcttta catcacttat 600

aacaatatat atttctgctt taatttgtaa tctttttttt ctgcgttgca acggaaatca 660

cgagcgatat atggtgaaga ctgatgataa tcgtatttct gatgacccat gattccgcgg 720

tgtaccatct gttctgtcaa ctaaaaagtg gagtagttcc ttgacggaag aagggagcaa 780

aatagaagat attctcagtt gatctgcagt tgttgttagg tcactatatt cagaaatcgc 840

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gcaaaactgt gccactggcg ccgaatacgt acggacagag ctcaggcaat caggggagca 1020

gcaaaagagg agagagttgg tgccaagcac aactaaaccc aactgcaccc aaaaactaat 1080

cagcatttca gttcgcttta gttagtacta ccacctgcat ctctttacca acactatata 1140

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tctaatcagt tcgcgtttgc taattaactc tgccatc 1237

<210> SEQ ID NO 11
<211> LENGTH: 1100
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: PR00116 - 26S proteasome regulatory particle non-ATPase subunit 11

<400> SEQUENCE: 11

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acctggtaga atatccccga gatcagtagt taccgtgatt ggttcagact tgagaggcta 120

atttttttcgt acctgtagct ttattacatc gcatttcctc ttattgaagt ttagccgagg 180

tggtgcggat ggatattcag tctaacagac tcaatgaacg ctttgttgta tgacttgtac 240

agtactggct gctcgaacag gatggttcag cttccagaaa tttggcaacg ctccatttca 300

aagaaaatca ttcagtattt gccttcttgt tgttacattg atctcatata aagtcacttt 360

gatcgttgac atcttgtttt ttggttcgtt tgccatggta gtttcccttg ctgctgggag 420

gattgccgcc tgaacttttt ctttttgcg aggatgttat ttttgccaga caagaacggg 480

aataagcaaa ttgtttggtg gaactaaagt aaactcgatc tctttccgag aagtgtatta 540

ttttcacgtg taccatcaat ttttttgaaa gtaaatattt ttccccttta actaatgttc 600

actttggacc ggataatctt acctttattt aactttgggc tatctaactc tcttctaaag 660

catataaacg atcttgagta catcgattcc tacttatcat ttaactctcg tagcttaatg 720

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taagattatt tctttgaaat atgataaatt ggatgcatat gaatgaaaga gtcaaggatt 780

aagtgattcc tcaaaaaaaa aaaagagtga aatttattta ttttttccct ttcgacacga 840

agaagggctt ggttggagga aaatggccca gattcagatg accgaggccg agtaccatgg 900

ggcccacaag aataataagc cccgagccca aacgctaagg cccacgagaa gccgtgcgct 960

ggaagaaaga aagaaaccgc ggccgtcttc acaccgaagc ggcggacgag acgactcgca 1020

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cgaagcgagc gagcggcggc 1100

<210> SEQ ID NO 12
<211> LENGTH: 1216
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: PR00117 - putative 40S ribosomal protein

<400> SEQUENCE: 12

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gaaatgtcat gtctatgctc cgatcttata aatttgttca atagcgttgc aaacgcgatc 120

attaaaaagg cggtaagaga actaccacat tttcgaaagc ccattctctt cgtgagttac 180

tggaattatt tggcatagca catgcataaa gatgctttag taatgagctc aataaaacac 240

gacagctttg catgtagcca caatgctata gtaaatgagt tgtacttctt ttgcattgca 300

aagtggtact gaccttgttt aggcagctag cttcattcat tttttgaatt ctatagttat 360

agttataaag attatcataa tttagataag aatccggtat gtttgagaag ctggagtttc 420

tagagaagct ataacaactc gaagctccct aaacagagcc attgaacatt gagctgtcca 480

gtatatcatg acaaaatgat acattttgca tgggcatatg tgtctaagaa aacaaacatc 540

acaattcaat gagtcactct aaaaaaaaag gcaaaacact caacaaaacc ataccgtgaa 600

agtgaaccta taatgaaatg aaattttgat aagcatgctt acccaggtgg aaatttcaat 660

ctaagaacaa tttccaaaac caccgtccat agaaatatgt ggaattcatt cagaattttc 720

ataccacacg ataaaattta tagggaattt aacttttgcc atttttaccg aacaccacct 780

tttcatttgc tcctataatg ttatcgaaaa gagagtgttt gttaattatt tgtcactttt 840

atcacgacat gtagccgtga caacgtggcg ttcctcgtgg agcccacccg tcagccgccg 900

tacgcaccac catcaaagaa ttcaagacgg agagcgtcgt cgccgtcggc aaggcggcgt 960

gttttgttca ctgtacgttg cttcggcgtg ggcccaatct tgttcgggcc taactagttc 1020

ttcccagccc aggcccatta agcctaccaa cccggacggc ccgggaggag ctagggtttc 1080

acccttcact atataaacct ctctctcctc ctccggccgc cgcctccgaa gccctagctc 1140

ctcccgccgc cgccgccgcc gccgccgccg cctctccact cgagagaccc agccgccgcc 1200

gccgccgccg ccgcca 1216

<210> SEQ ID NO 13
<211> LENGTH: 1210
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: PR00122 - chlorophyll a/b-binding protein
presursor (Cab27)

<400> SEQUENCE: 13

cagatgccac agtatggtgt accaccagct gctccacacc atgctccacc ggctggccaa 60

ccaatgtatt tcccgaaata atctatcttt atccgatgta caagcaatta gagcaattgc 120

aaatgttgcc tgcaatactc gggtctgggt atcttctctt caaattttgg gttgtaactc 180

gtctatgcag ctattcatat tgtaactcag tgagctccct gtcgcaaatg tgcctctgcg 240

tcagtcgctg tctgtaaact gtccggcaat tagaaattcc catccttagc atgcctggta 300

ttgttcagct cgaaactgaa atttttcttc gtgccctata ttttttcggt gtagataagt 360

gttccgctgg aattttatgc aggtgctgta ccctatgtgc tgctttttt ttgtgtgggg 420

cgccccccg gggggggggg ggggtttcct ggcatgattg caaataagaa ccccggggca 480

aatctgctgg ttggttgcaa ataataaccc ctccaaatct gcgcagatga aaccccattc 540

aggacatgaa ttacgattgt tcatgagcta tttggatcat ggaaagattg gaaacaaaca 600

cttacgtcaa ggtttctact aattacgtga ttccgatttc agagtcagcc atggctatac 660

tgcctttgct ccagtaaaca tcgctgctct agtaacaaac attgcagtaa acatcacaac 720

tatccaattc ccttgttgct gctctagtaa aaaacattgc aattatccaa ttcccagata 780

ttttctttca ctactccaaa acctaaagta catatacgtg agttgagtga tccagcaaca 840

taaaaatccg aggctccgag cgatctgcac caaccatctc acccgtccga cgtggcagca 900

gcaaccagcc acagctgaga cctccatcca atagaaaccc tccctttgat tcccccgtat 960

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tcgccaccgt ggccacctgg cagcgccggc cactcccgga cagtttaata caagccacgc 1140

ctttgctccg tgccggccaa aacgtaccct tgtgactaca cccgcttcgc ttcctcccct 1200

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<210> SEQ ID NO 14
<211> LENGTH: 1179
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: PRO0123 - putative protochlorophyllide reductase

<400> SEQUENCE: 14

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cattaccact ttacctgaca ttttggacag agattagaaa tagtttcgta ctacctgcaa 180

gttgcaactt gaaaagtgaa atttgttcct tgctaatata ttggcgtgta attcttttat 240

gcgttagcgt aaaaagttga aatttgggtc aagttactgg tcagattaac cagtaactgg 300

ttaaagttga aagatggtct tttagtaatg gagggagtac tacactatcc tcagctgatt 360

taaatcttat tccgtcggtg gtgatttcgt caatctccca acttagtttt tcaatatatt 420

cataggatag agtgtgcata tgtgtgttta tagggatgag tctacgcgcc ttatgaacac 480

ctacttttgt actgtatttg tcaatgaaaa gaaaatctta ccaatgctgc gatgctgaca 540

ccaagaagag gcgatgaaaa gtgcaacgga tatcgtgcca cgtcggttgc caagtcagca 600

cagacccaat gggcctttcc tacgtgtctc ggccacagcc agtcgtttac cgcacgttca 660

catgggcacg aactcgcgtc atcttcccac gcaaaacgac agatctgccc tatctggtcc 720

cacccatcag tggcccacac ctcccatgct gcattatttg cgactcccat cccgtcctcc 780

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acgcccaaac accgcacacg ggtcgcgata gccacgaccc aatcacacaa cgccacgtca 840

ccatatgtta cgggcagcca tgcgcagaag atcccgcgac gtcgctgtcc cccgtgtcgg 900

ttacgaaaaa atatcccacc acgtgtcgct ttcacaggac aatatctcga aggaaaaaaa 960

tcgtagcgga aaatccgagg cacgagctgc gattggctgg gaggcgtcca gcgtggtggg 1020

gggcccaccc ccttatcctt agcccgtggc gctcctcgct cctcgggtcc gtgtataaat 1080

accctccgga actcactctt gctggtcacc aacacgaagc aaaaggacac cagaaacata 1140

gtacacttga gctcactcca aactcaaaca ctcacacca 1179

<210> SEQ ID NO 15
<211> LENGTH: 1808
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: PRO0133 - chitinase Cht-3

<400> SEQUENCE: 15

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tgtaattata atatactttt aatcaaaaca tgcaaagcta gcagtattta catcactaga 120

agtaaatctt tcttgctcat gatgcttcag ccggacggaa ccctaaaata tagatggggc 180

ggatacactc gattaaaaca gctaattgca acacatatca tataaggttt tggaattcat 240

accaaatgct ccgaaattcg tctatttcga tgaggcccaa gacatgacct cctgtttcgc 300

ccatagttta tggtgtttgg taaaatttgg ttaaaatctg tctattttag taggtcccga 360

aattcttatg caattgaatc ctagaaccct atcatattta tattgcaatt gcacaaaaat 420

aatgtgcaat caatatattc caattgcaat acatatcaag catgaggtgt aatacatatc 480

cagccgctag cactgggtct gttgaggtgc ttcttgcagc aacagctgca atctgtttgg 540

ctaggctgtt ggcgccaggc actgctgtcg tgctgcaaca atggcacatt cgtcgagcac 600

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aactgatcag ttggctggat cgatggtatg tactagataa tatgcggtct aggcctagac 840

caagaagcag aagaggagtc gggtcgggag tgtggggcga cgtaggctgt agctgggccg 900

gccgccccag gccgcctaat gagtgtgtcc gcccctggcc tgacacgatg ggtaattaaa 960

tagttatgca tgtccctctt tgtctaaaca atatgtataa aattgacgat atcttgggca 1020

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tattgaacca aaaatcgact gtaatctcat gaaaattttc gtcataatta tagcaaaatc 1140

gttgttggat tgattgcacg agaaaacaga agaagggagc taggtgatat tatattgttt 1200

tgttgcctac ataaatctta aagcaatcga atggtctaaa atttacaaga tttttaaaga 1260

ggttttcgta ccgtatagac cccggccggg tcaaacttat ttggtcgtcg ctggttgttt 1320

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gagatcaatc tatcaatcgt caacccttg cctttgttag cgagctagcg tgtacacatt 1440

tcaattatat atggtgcatg catggcatcc acgcctccac ggtcaacgtg gaaatatctc 1500

tggaaactta ctttttctaa ataactgaac ggattggagg caggagacaa atttgaccaa 1560

cacaatatat ccacgacggc tagacaatac tagtagatgc atgcatggaa ggatatagta 1620

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gtacttgtta atcgtggaaa ctttggtaat gcgaatgcat ttcaattcgt tgctgaagat 1680

cgatgcacca tgcatatcca tctctatata aagccatgcg atcccaccga ttcttgcaca 1740

cacactagct acttctactt ctatcatacc aaacaaacta gcttaatttg cattgcatca 1800

cattgccg 1808

<210> SEQ ID NO 16
<211> LENGTH: 1828
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: PRO0151 WSI18

<400> SEQUENCE: 16

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tccggcttaa tgcttttctt ttgtcacata tactgcattg caacaattgc catatattca 180

cttctgccat cccattatat agcaactcaa gaatggattg atatatcccc tattactaat 240

ctagacatgt taaggctgag ttgggcagtc catcttccca acccaccacc ttcgtttttc 300

gcgcacatac ttttcaaact actaaatggt gtgtttttta aaaatatttt caatacaaaa 360

gttgctttaa aaaattatat tgatccattt ttttaaaaaa aatagctaat acttaattaa 420

tcacgtgtta aaagaccgct ccgttttgcg tgcaggaggg ataggttcac atcctgcatt 480

accgaacaca gcctaaatct tgttgtctag attcgtagta ctggatatat taaatcatgt 540

tctaagttac tatatactga gatgaataga ataagtaaaa ttagacccac cttaagtctt 600

gatgaagtta ctactagctg cgtttgggag gacttcccaa aaaaaaaagt attagccatt 660

agcacgtgat taattaagta ctagtttaaa aaacttaaaa aataaattaa tatgattctc 720

ttaagtaact ctcctataga aaacttttac aaaattacac cgtttaatag tttggaaaat 780

atgtcagtaa aaaataagag agtagaagtt atgaaagtta gaaaaagaat tgttttagta 840

gtatacagtt ataaactatt ccctctgttc taaaacataa gggattatgg atggattcga 900

catgtaccag taccatgaat cgaatccaga caagtttttt atgcatattt attctactat 960

aatatatcac atctgctcta aatatcttat atttcgaggt ggagactgtc gctatgtttt 1020

tctgcccgtt gctaagcaca cgccaccccc gatgcgggga cgcctctggc cttcttgcca 1080

cgataattga atggaacttc cacattcaga ttcgataggt gaccgtcgac tccaagtgct 1140

ttgcacaaaa caactccggc ctcccggcca ccagtcacac gactcacggc actaccaccc 1200

ctgactccct gaggcggacc tgccactgtt ctgcatgcga agctatctaa aattctgaag 1260

caaagaaagc acagcacatg ctccgggaca cgcgccaccc ggcggaaaag ggctcggtgt 1320

ggcgatctca cagccgcata tcgcatttca caagccgccc atctccaccg gcttcacgag 1380

gctcatcgcg gcacgaccgc gcacggaacg cacgcggccg acccgcgcgc ctcgatgcgc 1440

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tctctgtctt ttgctccccg gcgcgcgcca gttcggagta ccagcgaaac ccggacacct 1560

ggtacacctc cgccggccac aacgcgtgtc ccccctacgt ggccgcgcag cacatgccca 1620

tgcgcgacac gtgcacctcc tcatccaaac tctcaagtct caacggtcct ataaatgcac 1680

ggatagcctc aagctgctcg tcacaaggca agaggcaaga ggcaagagca tccgtattaa 1740

ccagcctttt gagacttgag agtgtgtgtg actcgatcca gcgtagtttc agttcgtgtg 1800

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<210> SEQ ID NO 17
<211> LENGTH: 1267
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: PR00169 - aquaporine

<400> SEQUENCE: 17

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atcatattat tttttataaa gttatcaaaa tgtacatata tttatttatt tttaccaaac 120

tttactaaat gagataatcc aacaaatggc atttaaagcg ttcaaatcca agaaatgcca 180

tcgccgttat gcttccgtcc gtttcacgcc gttaaaatac aatgttcatc ctataacact 240

taatggtgtg gaatggacgg aaccctaacg gcgatggcat ttttgggata aagtcgtttg 300

tacgatggca tttcttagaa ctcatatttg tcgatggcat tttttgaatt tggatgattg 360

tcaatggtat tttttggatt atctcttagt aaatacataa ggaatcatgc caaaacttga 420

caatattgtc aacttatcaa aatttaattg ggattatttt ggcgataata tgaacagccc 480

ttacatttct gaagaattat agctcaaata tggctatggc cctgtttgga ttcggagggc 540

tatttaatag ccctccggaa tcttgctatt taagagtatt aaacgtagat tactgataaa 600

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tgatttgcta cagtaatcag ccgctaatcg tggattaata tacatcatta gattcgtctc 720

gtaaaatagg ctagggatta tggaatcggt tttatcggta atctatgttt aatacttcta 780

aatagcaaga ttccgaaggg ctatttaata gctcggagca tccaaacaag gcctatgttt 840

agatccaaac ttccaacttt ttctatcaca ttaaactgtc atacatacat aacttttcag 900

tcacatcgta ccaatttcaa cccaaacttt caactttgga agaactaaac acagcatatg 960

acagtgcagt tcagctcaat tttgttcgga gcctaaaaaa aagaaaagaa aaaaagctca 1020

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accagggccc acgctccact cccgtgatca tcacctcctt ccctttccag aaccaccttc 1140

tccttccttc ctcctcttct tcttcagtgt actctgcctt tataacaccc tactcctctc 1200

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ggcgaca 1267

<210> SEQ ID NO 18
<211> LENGTH: 1130
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: PR00170 - High mobility group protein

<400> SEQUENCE: 18

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tatacaaagc tgtaatactc gtatcagcaa gagagaggca cacaagttgt agcagtagca 120

caggattaga aaaacgggac gacaaatagt aatggaaaaa caaaaaaaaa caaggaaaca 180

catggcaata taaatggaga aatcacaaga ggaacagaat ccgggcaata cgctgcgaaa 240

gtactcgtac gtaaaaaaaa gaggcgcatt catgtgtgga cagcgtgcag cagaagcagg 300

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gatttgaaac cactcaaatc caccactgca aaccttcaaa cgaggccatg gtttgaagca 360

tagaaagcac aggtaagaag cacaacgccc tcgctctcca ccctcccacc caatcgcgac 420

gcacctcgcg gatcggtgac gtggcctcgc cccccaaaaa tatcccgcgg cgtgaagctg 480

acaccccggg cccacccacc tgtcacgttg gcacatgttg gttatggttc ccggccgcac 540

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cggccccgcg cgtcatcgcg gggcggggtg tagcgggtgc gaaaaggagg cgatcggtac 780

gaaaattcaa attaggaggt ggggggcggg gcccttggag aataagcgga atcgcagata 840

tgcccctgac ttggcttggc tcctcttctt cttatccctt gtcctcgcaa ccccgcttcc 900

ttctctcctc tcctcttctc ttctcttctc tggtggtgtg ggtgtgtccc tgtctccccc 960

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<210> SEQ ID NO 19
<211> LENGTH: 1230
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: PRO0171 - reversibly glycosylated protein RGP1

<400> SEQUENCE: 19

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tcataaaata gtaatcatgt tctccataac agtaaatgac gaggcgttaa tagtggttta 180

ggttctcatg attgtaaatg ttgagtcgct tgtagcggct taagatatag tagagagtat 240

atctagtttt atcaagacaa acattgcgta atgcctcgga cctaatataa aagtaggaat 300

tttaaccttt gagaaactgt aaccaattga aactgcaagc tttaaaaaaa catctattgg 360

aagtgatatt atatagacaa aataagtttc ttactcttac tctctcagtt tcaagttata 420

aaatgttttg gctttggtca aaatcaaact tcttcaagtt taatcaagtt tatagaaaaa 480

atagtaatat ccaagataaa tttattataa aaatatattt aattattatt ttaataaaac 540

taatttggta atgtaaatat tactatattt gtctataaac ttagtcaaat ttaaaacagt 600

ttaactttga ccaaagtcaa aacatcttat aacctgaaat ggatggagta tttgtttgtt 660

tctattttag gaaacggccg tttctttcca ttgattttga gataagcaga gctttaaacc 720

actgccacta ttgtgcattt catttgattt aacacttta ccccttatct ccaataaaaa 780

cgatattaag ataccctat cttttatcca ccgcttggaa caaaccaaaa aaaataaaaa 840

ttcaaacctt ctacactggt acacacgttc tctctttcca tgcaccgaca ggtctctccc 900

agatccaacc caaaataaat ttggacgcat cccaaaattc ggcaaacata tgacgcaaac 960

caaaacaaaa taggcacaaa ataatataat actcctatct aattaattat acacaatttt 1020

ttttaaaaaa aaagcaaggc aagcgaagca aagcaaagaa ggaaacgaat aacaaagtcg 1080

tcgtcctccc ggagctcccg ctctataaat cgctcctcct ccccacccac ccaaacccac 1140

acacacctca cacctcacca ccatcacctc ctcctcctcc tcctcttcct ccgcgcgcgc 1200

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gagatccagg gagagggaga gggagagatc 1230

<210> SEQ ID NO 20
<211> LENGTH: 1234
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: PRO0173 - cytosolic MDH

<400> SEQUENCE: 20

gtttggttgg tgaccgcaat ttgctatacc aaaatcttag acacagttga attaagctac 60

actttattag cacattggcc cgtgcgttat attgtcattt tctagccaaa gtttgccata 120

attgtggcta acaaattgtt ggccacattt tggctacgtt cgataggaca tgttcccaac 180

ttctccttct cgtttttcgc gcgtacgctt tttcaaactg ttaaacggtg tgtttttttgc 240

aaaatatttt tttacgaaag ttgcttaaaa aattatatta atctattttt tttaaaaaaa 300

gtagctaaaa cttaattaat ctcacgctag acgctgcttc gttttacgtg tcgggtaccc 360

aaccctcact cccgaacaca gcctttgtgt ggtttactac agttatagta aagctagtct 420

ccatccaaac aatcctttag tccatataac ttcgtatact ccaaaattcc actcgttcta 480

cggacatcac taatacgaag atcaagtgga agatagatat ttttaatgac atgttatttt 540

cagtgaacac ttgaggtcct cacgatccac aaacacacat tttcgtagat aagttctgaa 600

atactccata cggcggttgt cacgatgtca tgatcgtcgt tacccaagga agaagaaaag 660

agtggcatct tctccacgcc agtgttccca acggagcatc ttttcttccc ccacacggca 720

tcgacgtcac actttctggt gcaaacttta ataattagtc caaaaacaaa aaaagaattt 780

cggccacatc ttctcccgaa acgccaggtg ggccccacct gcatcactga cagcctgtcc 840

ccacaacgcg cagtcgtgtc cccacctgtc aggatgttag cgtctccgtt gcaggtttcc 900

cagatcccat cgccgatctg tgggccagcg cccacggtgt cacgcccgcg cacacctggc 960

tccaacccac ccaccccacg cgctccgtgg ccgacagcgt ggacccacct aggtggggcc 1020

caccgtcagt gggagatggg taggggagcc cccacgtggg agcaacgggg gttctccggg 1080

ctccccgtcg ccgcgaggtt aaataacggc cacccgtttc cccctctctc gcaaaactca 1140

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tcgaagctcc cgctcccccc ccccttccgc tcca 1234

<210> SEQ ID NO 21
<211> LENGTH: 1553
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: PRO0175 RAB21

<400> SEQUENCE: 21

gtcaccaccg tcatgtacga ggctgcttca ccactgcctc actgccacca gcgtctcccg 60

ccgcgtgcaa tacaagaaga aacatcgaac ggtcatataa ggtaagaccc actaccgatt 120

taacctatca ttcccacaat ctaatccact tatttctctt cccatgatct tatcctctca 180

tttctcctca ctacttttgc atttgtagga aacacaatga caccgtcgaa gaaagctggt 240

ggagcaccgt agccagcaat caccaaaaca cagaggggag gaggtcggca gcggccatgc 300

ggacggcgat gagacaacgc gacgcaaaga gggaggagga cgttggcgat catgctggtg 360

ttggcggagg aggtcactgg ccatgcgaat gacagcgggg cagcgcaaca caaaaagggg 420

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ggaggatgcc ggcgaccacg ctagtaccat gaagcaagat gatgtgaaag ggaggaccgg 480

acgagggttg gacctctgcc gccgacgtga agagcgtgat gtgtagaagg agatgttaga 540

ccagatgccg acgcaactta gccctgcaag tcacccgact gcatatcgct gcttgccctc 600

gtcctcatgt acacaatcag cttgcttatc tctccatact tgtcgtttgt ttcccgtggc 660

cgaaatagaa gaagacagag gtgggttttg ttggagagtt ttagtggtat tgtaggccta 720

tttgtaattt tgttgtactt tattgtatta atcaataaag gtgtttcatt ctattttgac 780

tcaatgttga atccattgat ctcttggtgt tgcactcagt atgttagaat attcattccg 840

ttgaaacaat cttggttaag ggttggaaca tttttatctg ttcggtgaaa catccgtaat 900

attttcgttg aaacaatttt tatccgacag caccgtccaa caatttacac caatttggac 960

gtgtgataca tagcagtccc caagtgaaac tgaccaccag ttgaaaggta tacaaagtga 1020

acttattcat ctaaaagacc gcagagatgg gccgtggccg tggctgcgaa acgacagcgt 1080

tcaggcccat gagccattta ttttttaaaa aaatatttca acaaaaaaga gaacggataa 1140

aatccatcga aaaaaaaaaa ctttcctacg catcctctcc tatctccatc cacggcgagc 1200

actcatccaa accgtccatc cacgcgcaca gtacacacac atagttatcg tctctccccc 1260

cgatgagtca ccacccgtgt cttcgagaaa cgcctcgccc gacaccgtac gtgcgccacc 1320

gccgcgcctg ccgcctggac acgtccggct cctctcccgc cgcgctggcc accgtccacc 1380

ggctcccgca cacgtctccc tgtctccctc cacccatgcc gtggcaatcg agctcatctc 1440

ctcgcctcct ccggcttata aatggcggcc accaccttca cctgcttgca caccacagca 1500

agagctaagt gagctagcca ctgatcagaa gaacacctcg atctctgaga gtg 1553

<210> SEQ ID NO 22
<211> LENGTH: 1087
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: PR00177 - Cdc2-1

<400> SEQUENCE: 22

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atgacttggg tctagtgatg gaagtggata gttccactac ctacataaaa acccactact 120

agtttattac ttttcacatg atagcataaa atttaaagaa aaaataaaca gaagtggaat 180

aagcgaaaaa ccccgcttac ccgccccatt tacatcccta cttggatcct gcatgtcagt 240

aagatatcag aattatatgt tttagaatta tatgtttttt tggaaggtgg aaatcggatt 300

attagacgca acataccaag tggcgtatac ttggcttcac tctttccatc agagcaagcg 360

taaaagatca cgtattcacg tcacatggag taactgagcg aatttttttc atttttaaat 420

ttttgttttt taatatttac ataaatatta taccggcgaa aatatttaca aaagtagacc 480

ctgctgccct tctccttctc gagaagagcg gcagggtgat gtcagggaca gaaataaact 540

ccaaaaatgc atttttggct gggcgaaaat tgcacttacc cccttgctgc cctctacaaa 600

ggttgcaagg gacctcagtg caaaatacgc acaccttgcc gtcctccact tggacggcat 660

gggctatttc tgtaaatatt ttggatggta taatatttct gtaaatatta aaaaataaaa 720

atttaaaaat gaaaaaattc tatctgggct cccttctctc atctcacacg gcccaccaca 780

caatcccggc ccacatattt cctgggccca tttccgtgtg aatggagacg gcccattggc 840

gcgcacatgc ggaaaagcgt acacacgatt cgaaatttga aatctcaaaa agcgcccgtt 900

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agagcgcgtc ccctccaacg gctatcccca atacaaaaga tcactcgaat ccccccaaa 960

tcgaccaaac cctaaatcca cgcgcattcc acaccaccca accagcgaga gagagatggc 1020

ggcgctccac caccaggcgg cggcggcgcc ggtgacgacg acgacggacg ggggcgagct 1080

gcgggcg 1087

<210> SEQ ID NO 23
<211> LENGTH: 1272
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: TC89946 (PRO0110)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (17)..(17)
<223> OTHER INFORMATION: n = any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (50)..(50)
<223> OTHER INFORMATION: n = any nucleotide

<400> SEQUENCE: 23

tttgacgact gaatcgnggc tcgcctctgc ggcggccgct ctagattagn gtttcccctg 60

tctgttgtaa ttcggcacga gggctgatca agagctctta attagctagc tagtgattag 120

ctgcgcttgt gatcgatcga tctcgggtac gtagcaatgg cgtccaaggc gttcgctctg 180

ttcctggccg tgaacctcgt cgtgctcggg gtggcaagcg cctgcggcgg cagcccgtcg 240

tgcccgacgc cgacgccgtc gaccccgaca ccgtcaacgc cgacgccgac gccgtcggcg 300

ttcgggaggt gcccccgcga cgcgctgaag ctgggcgtgt gcgccaacgt gctgggcctg 360

atcaaggcca aggtgggcgt gcctccggcg gagccgtgct gcccgctgct ggaggggctc 420

gtcgacctcg aggcggcggt gtgcctctgc acggccatca ggggcaacat cctcggaatc 480

aacctcaacc tccccatcga cctcagcctc atcctcaact actgcggcaa gaccgtcccc 540

accggcttca agtgctaagc agcgtgcata tgcaatgcct gcatgggttg atcctacgta 600

cggtgattag ttggctttga cgactcttga tttgatttgc ttgctgctct gtttatttgc 660

tactacgtta cgtacgtact ttgcatgcaa cgcaacgcat gatcgatcgt gcatgctggc 720

tgtttgtacg tatcacggta ccagtttgga ttctctctgt actctctcct ttgtcttctt 780

tgtagtactc ttattcccgc tatccgtacg tgcgcatttg ttgtaagggc cggtgctagc 840

ttgtgtgccg gtaccaactt ctaataaagc tatgggtgga acttcaaaaa aaataaaaaa 900

aaaactggag ggggggcccg ggtccaattt agactataat gagtttaaca ccccgctcat 960

cggccgaaga taacaacacc gggcttggaa aacctagact gcccaactaa tggacggaag 1020

acagactctt ggactgaaac tgaacgaaac aagaccaccc accccatcta accacagcca 1080

cctaccgcca aagattccaa taatgtgaat cagtcggtaa tagaacactc ctcttgtacg 1140

attttactgc ccgcgccacc cctcggtacg cacttatata tatcgggccg tagtaatttc 1200

ctggttccgt cacttccctc atcgcacctg ctagtcgtgg cttacatacg tgcgtcctct 1260

tattatcgag cg 1272

<210> SEQ ID NO 24
<211> LENGTH: 2425
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa
<220> FEATURE:
<221> NAME/KEY: misc_feature

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<223> OTHER INFORMATION: TC90358 (PRO0005)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1558)..(1558)
<223> OTHER INFORMATION: n = any nucleotide

<400> SEQUENCE: 24

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cccaatcccc aacctcccaa taatccgatc tctcccagtt ctgttcggat caaggctgtg 120

tcgatcgcaa aaaagaaaaa aaaaacaatt tccttttggg gtggttcatc tgttgatcac 180

ttctttgttt cccgcgtttt gttggggatt cgattttcgg gttaagattt tctacacgat 240

ggccttgaac ttggctcaga gcgccgcggc ggcagcgtgc ttcgcgaccg ccggtgatgc 300

gcggcgagct gcttcggtgg tcgccatgcc gtcgtcgtcg tcgtcggcca cgacgagcct 360

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ggcggcggcg gcggcgagca gcaggaggaa cggcgtgccg gtgttcgtga tgatgccgct 480

ggacacggtg agcaagtgcg ggagcgcgct gaaccggagg aaggcggtgg cggcgagcct 540

ggcggcgctg aagagcgccg gcgtggaggg gatcatggtg gacgtgtggt ggggcatcgt 600

ggagagcgag ggccccggcc ggtacaactt cgacggctac gtggagctca tggagatggc 660

ccgcaagacc ggcctcaagg tccaggccgt catgtccttc caccagtgcg gcggcaacgt 720

cggcgactcc gtcaacatcc cgctcccgag gtgggtggtg gaggagatgg agaaggacaa 780

cgacctcgcc tacaccgacc aatggggacg ccgcaacttc gagtacatct ccctcggctg 840

cgacgccatg cccgtcttca agggccgcac gcccgtcgag tgctacaccg acttcatgcg 900

cgccttccgc gaccacttcg cctccttcct cggcgacacc atcgtcgaaa tccaagtcgg 960

catgggcccc gccggcgagc ttcggtaccc gtcctacccg gagagcaacg gcacctggag 1020

gttccccggc atcggcgcct tccaatgcaa cgacaggtac atgcgtagca gcctgaaggc 1080

ggcggcggag gcgaggggca agccggtagt ggggccacgg cgggccgacg gacgccggcg 1140

gctacaacaa ctggccggaa gacacggtgt tcttccgcgg cgactgcggc gggtggagca 1200

ccgagtacgg cgagttcttc ctgtcgtggt attcgcagat gctgctggag cacggcgagc 1260

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aaaaaacgca gaaatgcgtt gtgttcttgc gctctggttc gttgctgctg tgggtcagat 2220

tcagctggtg aaaaaactac agtactactg aaactgaaac tactagagcc tagagggaga 2280

ttaagctaag ttaattgcac gagtaattac tccacggttg tgtttagggt ctacgtcggc 2340

agattttgct ttctggtaga tccctaacct tatgtttgtt gggaatttta taaaggagct 2400

aagtttgcct attgatttgc aatct 2425

<210> SEQ ID NO 25
<211> LENGTH: 3410
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: TC83635 (PRO0009)

<400> SEQUENCE: 25

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actaccccgt cgaccgcgtc tcctgctacg tctccgacga cggcgcgtcc atgctgctct 1020

tcgacacgct ctccgagacc gccgagttcg cccgccggtg ggtccccttc tgcaagaagt 1080

tcaccatcga gccccgcgcc cccgagttct acttctccca gaagatcgac tacctcaagg 1140

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tgtacgtgtc ccgcgagaag cggcccggct acaaccacca caagaaggcc ggcgccatga 1440

actccctcgt tcgcgtctcc gccgtgctta ccaacgcccc cttcatcctc aacctcgact 1500

gcgaccacta cgtcaacaac agcaaggccg tccgcgaggc catgtgcttc ctcatggaca 1560

agcagctcgg caagaagctg tgctacgtcc agttccccca gcgcttcgac ggcatcgacc 1620

gccacgatcg ctacgccaac cgcaacaccg tcttcttcga catcaacatg aaggggctgg 1680

acgggataca ggggccggtg tacgtgggga cggggacggt gttcaacagg caggcgctgt 1740

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acggatacga cccgccgcgg ccggagaaga ggccgaagat gacgtgcgac tgctggccgt 1800

cgtggtgctg ctgctgctgc tgcttcggcg gggggaagcg cggcaagtcg cacaagaaca 1860

agaagggcgg cggcggcggc gagggcggcg gcctcgacga gccgcgccgc gggctgctcg 1920

ggttctacaa gaagaggagc aagaaggaca agctcggcgg cggcgcggcg tcgctcgccg 1980

gagggaagaa agggtaccgg aagcaccagc gcgggttcga gctggaggag atcgaggagg 2040

gcctcgaggg gtacgacgag ctggagcgct cgtcgctcat gtcgcagaag agcttcgaga 2100

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cccagggcgc cgccgccgac cccgccgccc tcatcaagga ggccatccac gtcatcagct 2220

gcggctacga ggagaagacc gagtggggca aggagattgg gtggatctac gggtcggtga 2280

cggaggacat cttaacgggg ttcaagatgc attgccgtgg gtggaagtcg gtgtactgca 2340

cgccggcgag ggcggcattc aaggggtcgg cgcccatcaa cctgtcggat cgtctgcacc 2400

aggtgctccg gtgggcgctc ggctccgtcg agatcttcat gagccgccat tgcccgctct 2460

ggtaccctat ggcggccgcc tcaagtggct cgagcgcttc gcctacacca acaccatcgt 2520

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cgtgttccaa ggcctcctca aggtgctcgg cggcgtggac accaacttca cggtgacgtc 2820

caaagccgcc gccgacgaag accgacgcgt tcggcgagct ctaactgttc aagtggacga 2880

cgctgctggt gccgccgacg acgctgatca tcatcaacat ggtggggatc gtcgccggcg 2940

tgtcggacgc cgtgaacaac gggtacgggt cgtggggccc gctgttcggg aagctcttct 3000

tctccttctg ggtcatcctc cacctctacc ccttcctcaa ggggctcatg gggaggcaga 3060

accggacgcc cacaattgtc gtgctctggt ccaacctcct cgcctccatc ttctccctcg 3120

tctgggtcag gatcgacccc ttcatcccca agcccaaggg ccccgtcctc aagccatgcg 3180

gggtctcgtg ctgagctgct gctgctactt ctctgtgtct ctgcattttg caagagggat 3240

gaccggatgg atgattcttg ttgtatggag tattttgact tgttcatgta caagtttttg 3300

tgagtgggat aaaagtgttt tgggggtaaa atttgtaaga actgaggtgg agattatact 3360

cgaatttaag aacaattgtt tttgaatttt cttttaagat ttttgggagt 3410

<210> SEQ ID NO 26
<211> LENGTH: 602
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: TC83117 (PRO0058)

<400> SEQUENCE: 26

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atggaggctt cacgcaaggt gttctcggcc atgcttctca tggtgctgct gcttgcagcc 120

actggtgaga tgggcgggcc ggtgatggtg gcggaggctc ggacgtgcga gtcgcagagc 180

caccggttca agggcccgtg cgcccgcaag gcgaactgcg ccagcgtatg caacacggag 240

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ccctgatcga tgaaccagca gctagcgcag cagcttgtgc cgccacctcg cgcatgtgtc 360

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cgtggttttc tcttggagaa ctttggcttt tgtggtgtta agttcgatcg ttttgtgcat 480

ccaccatcca tccatcctcc cattctgctt gttctaaggt tatactacta cttgagaagg 540

tgatgcaatt gtgctcaaca gtttattaat acttcatccg ttttaaaatg tttgaccccg 600

tt 602

<210> SEQ ID NO 27
<211> LENGTH: 1170
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: TC89913 (PRO0061)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (15)..(16)
<223> OTHER INFORMATION: n = any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1162)..(1162)
<223> OTHER INFORMATION: n = any nucleotide

<400> SEQUENCE: 27

aattcggcac gagannaaaa ggaaaaaaaa acaaaacaca ccaagccaaa taaaagcgac 60

aatgggatcg ctcaccacca acatcgtcct cgccgtcgcc gtggtggcag cgctggtcgg 120

cggcgggtcg tgcggcccgc ccaaggtgcc acccggcccg aacatcacga ccaactacaa 180

cgccccgtgg ctccccgcca gggccacctg gtacggccag ccctacggct ccggctccac 240

cgacaatggt ggcgcgtgcg ggatcaagaa cgtcaacctg cctccctaca acggcatgat 300

ctcctgcggc aacgtcccaa tcttcaagga cggcagggga tgcggctcat gctacgaggt 360

gaagtgtgag cagccggcgg cgtgctcgaa gcagccggtg acggtgttca tcacggacat 420

gaactacgag cccatctcgg cgtaccactt cgacttctcc ggcaaggcgt tcggcgccat 480

ggcttgcccg gggaaggaga ccgagctccg caaggccggc atcatcgaca tgcagttcag 540

gagggtgcgc tgcaagtacc ccggcggcca gaaggtcacc ttccacgtcg agaagggctc 600

caaccccaac tacctcgccg tgctcgtcaa gttcgtcgcc gacgacggtg acgtcatcca 660

gatggacctc caggaggccg gattgccagc gtggaggccc atgaagctgt cgtggggcgc 720

catctggagg atggacaccg ccacgccact caaggcaccc ttctccattc gcgtcaccac 780

cgagtccggc aagagcctca tcgccaaaga cgtcatcccg gtcaactgga tgccagacgc 840

catctacgta tcaaacgtcc agttctattg agatcggacg gaaacgatcc tcctaattta 900

tttccctatt aatttgttca aatggtttcc ttctataacc tatatttttc ccgttgttag 960

aaatggttcc atttcctcct acagcttact ttaagatagt tgcgcttgta tatctgcgcc 1020

atcttgtaag ttgtaagatg ctgaagaaca ctatgaattc tgagcatctg attctccggg 1080

aagatttact atgataaaca acagtttgat ttactatgtg tgtccccttg tttattgtat 1140

gctatcctaa tacttatgaa angttttgat 1170

<210> SEQ ID NO 28
<211> LENGTH: 861
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: TC89985

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<400> SEQUENCE: 28

ccacgcgtcc gcccacgcgt ccgcgatcag cagcagcagc agcttgcaca ctcgagctta 60

gcttagcttt tgcaagagag atcgagctag agatggagaa gtcgagcaag atgatggcgg 120

tggcggcggt gctggtgctc gcggtggtcg gcgcggcgga ggcgaggaac atcaaggcgg 180

cggcggcggc ggcggcggag agcaaggaca cggtggtgca gccgacgacg ttcccgccgt 240

tcgaccgctt cgggagcgcg gtgccggcgt tcggcggcat gcccggcagc agcatcccgg 300

ggttcagcct ccccggcagc agcggctcca cccccggcgg cctcggcggc ttcggcagca 360

tgcccatgtt cggcggcctc ggcggcggct cacctggcct cggcggcggc atgcccggct 420

cccccgccgc cgccgacaag caggccaaga agccatgaga gacctcgccg tcgccggcgg 480

cgtcgccgct gctgcgcggg taatgtgctc tatgtagcgc acggcgttgc atgcaatatg 540

gatggctata tgacgcgcgc gcgttatatc ttcatatgtg cagttagctt gcactgtgtc 600

tagctagcgt tctattatga gtagtgtctc ttctatctct tttctttaca tgcatttgga 660

ggaggattat tctatctgtt tgttggttgg ttgtgtttgt ttgttttaat taggtccctt 720

cttatatttt gtgttttaat taagttcgtg atcatgtagt agtactacca ctgtttcgag 780

ctcgaggcat gaataatgct aaatgtgatc attattgtgt tattgtatgg tgatggctat 840

atatattact atctctgctt c 861

<210> SEQ ID NO 29
<211> LENGTH: 1252
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: TC89891 (PRO0081)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (5)..(5)
<223> OTHER INFORMATION: n = any nucleotide

<400> SEQUENCE: 29

cccangcgtc cgaaccaatc gactcgcacc accaccagca gctcaagcag caacagctca 60

aacggaggaa gatctcatcg ccatgacgac cggcaatggc gacgcaccgg tgatcaagaa 120

cgcccacagc gacatcgaca gcaccaacaa gacgctgctc aagagcgacg ccctgtacaa 180

gtatgtcctg gacacgacgg tgctgccacg ggagccggag tgcatgcgcg atctgcgcct 240

catcacggac aagcaccagt gggggttcat gcagtcgtcg gcggatgagg cgcagtgctg 300

gggatgctgc tgaagatggc cggagcgaag aggacaatcg aggtgggtgt cttcaccggc 360

tactcgctgc tggcgacggc gctggcgctg ccggaggacg ggaaggtggt ggcgatcgac 420

ccggacaggg agagctacga gatcgggcgg ccgttcttgg agaaggccgg ggtggcgcac 480

aaggtggact tccgcgaggg gaaggggctg gagaagctgg acgagctgct cgccgaggag 540

gcggcggcgg ggcgcgaggc ggcgttcgac ttcgcgttcg tggacgcgga caagcccaac 600

tacgtcaagt accacgagca gctgctgcag ctggtgcgcg tcggcgggca catcgtgtac 660

gacaacacgc tgtgggccgg cacggtggcg ctgccgccgg acacgccgct gtcggacctg 720

gaccggaggt tctccgtcgc catcagggac ctcaactcca ggctcgccgc cgacccgcgc 780

atcgacgtct gccagctcgc catcgccgac ggcatcacca tctgccgccg cctcgtgtga 840

ggtcgagacc gagaccttac cggccgatcc atccatcgct ctcgcgtgat taattaacgt 900

gtgttgctgt actcttctac tgctacaact atactattac ttccttaatt gccgcttaaa 960

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ttttcctata cgtgtttcaa tcaatgagat tattatattc ttcgagcatg agagagacgg 1020

agttgtaggg acatttgatg atggttgtta ctgtactaca tgttgataag tgcaacatct 1080

ctttccatgg ttgctactct actcaccgtg tcatgttggt tgcggatttt gatctcatct 1140

gcaagatgga ctactggggc ccaaaatgga acagactggt ccctcgatcc tgcaggagct 1200

tgcacctgtt gcaagggcct ttttaactgg ctaactaggt gggtaagtag gg 1252

<210> SEQ ID NO 30
<211> LENGTH: 671
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: TC89670 (PRO0091)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (3)..(3)
<223> OTHER INFORMATION: n = any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (14)..(14)
<223> OTHER INFORMATION: n = any nucleotide

<400> SEQUENCE: 30

gcnggcttcg gcangagttc aaacattata gttgaagcat agtagtagaa tcctacaaaa 60

atgaagatca ttttcgtatt tgctctcctt gctattgttg catgcaacgc ttctgcacgg 120

tttgatgctc ttagtcaaag ttatagacaa tatcaactac aatcgcatct cctgctacag 180

caacaagtgc tcagcccatg cagtgagttc gtaaggcaac agcatagcat agtggcaacc 240

cccttctggc aaccagctac gtttcaattg ataaacaacc aagtcatgca gcaacagtgt 300

tgccaacagc tcaggctggt agcgcaacaa tctcactacc aggccattag tagcgttcag 360

gcgattgtgc agcaactaca gctgcagcag gtcggtgttg tctactttga tcagactcaa 420

gctcaagctc aagctttgct ggccttaaac ttgccatcca tatgtggtat ctatcctaac 480

tactacattg ctccgaggag cattcccacc gttggtggtg tctggtactg aattgtaata 540

gtataatggt tcaaatgtta aaaataaagt catgcatcat catgcgtgac agttgaaact 600

tgatgtcata taaatctaaa taaaatcacc tatttaaata gcattcatgt atgagttcca 660

ttatcatagc t 671

<210> SEQ ID NO 31
<211> LENGTH: 436
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: TC89883 (PRO0095)

<400> SEQUENCE: 31

cctcgagggt cgacccacgc gtccgctctc ctctcttctc tcgccctcac cgctcgccga 60

ggttgccgtc tccttgtctc ctccgctcct tgcgccgccg ccgcgacgag tcgcggggag 120

gggcggcgat ctccatctcc atctgaggcg aggagagcag gggaggtgag gggatcctgg 180

tgaggtttgt gattactgga caatagaaat atttacacaa tatggctggc ggctctgctg 240

atgcagtgac caaggagatg gaggcgctac tcgttggaca aaatccaaat gcggttagtg 300

gagaaacatg cgagacctca tcaaaagaag gcaaagttgc agatagcaat ggatctcatt 360

cttcaccacc agaagatgat gatgatgaag cgcaagggga tggtccatct caagattgga 420

ggatccagaa gctttc 436

<210> SEQ ID NO 32
<211> LENGTH: 860
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: TC90434 (PRO0111)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: n = any nulceotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (10)..(10)
<223> OTHER INFORMATION: n = any nulceotide

<400> SEQUENCE: 32

nagggctaan attaccggag tatttttgca aagggagtaa tcaaagttcc aatacgaaat 60

cgcggtcgta gtagtacaat acaaagacga gttcacggag cgcgtaaact aataaggaaa 120

aattaaacgt cgcggagaaa taatagccga actggatgaa gatgagcagc actgcctctt 180

gcctagccta gcccatcatg gcgaggccga cggccccgac cagcaggccc atcaccgaac 240

gggcctcgct gccgctggcc ccgccggtgc tgcccgtcga cttcgtcgtc gtcgtcgtcg 300

gcgtcgtggt cgcgtccggc gtcgacgagg gcgtgtccat gccggggtcc gatgacggcg 360

tggcgggcgt cgcggtggac ggcggggacg acgacgccgt cggggtgggg gtggtgccgg 420

ccgccgcgga gaccgtgacg gcgagcttca tgccgccgga gcagtggccg ctggtgccgc 480

agatgaagta gcgggtgccg ggcttggtga gcgcgatctt ggtgttctgg tcgctgtagg 540

actggatcga gttgctggcg gacacgcgct gtagtcagcc gagctcacct ccgccaccgt 600

gtgcatcatg ctgtactgga acacgagcga gtcaccaacg ctgaaggttt tgctcttcgc 660

ccaggtatcg tagtccacgc cactgctcca gccggatgtg tcgccgacgg tgtagtccac 720

ggcgaaagcc ggcgcaacgg cggcgaggag tagcaccacc agacctgcag ctgcaagtcc 780

atgtactcca gccatgatgg cagagttaat tagcaaacgc gaactgatta gagccgtact 840

agtactggtg gccctcgtgc 860

<210> SEQ ID NO 33
<211> LENGTH: 1167
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: TC83072 (PRO0116)

<400> SEQUENCE: 33

aggaaaagaa gaaaaaagat cctgtgaacc ctacgaaact accgaagcga acggaaggca 60

ggaatcggcg gcggcggcgg cggcggcggt ggggagaagc catggagcgg ctgcagcgga 120

tcttcggcgc ctccggcatg gggcagccgc cgtcggactc gccgctgctc gactcctccg 180

agcaggtcta catctcctcc ctcgccctcc tcaagatgct caagcacggg agggccggcg 240

tgccgatgga ggtgatgggg ctgatgctgg gggagttcgt cgacgactac acggtcaggg 300

tggtcgacgt cttcgccatg ccgcagagcg ggaccggggt cagcgtcgag gccgtcgacc 360

atgtcttcca gaccaacatg ctcgacatgc tcaagcagac cgggaggcca gaaatggtgg 420

taggttggta ccattcccat cctggatttg gttgctggct ttcaggagtt gacatcaata 480

ctcaacagag ttttgaagct ttaaacccca gggcagttgc cgtcgtgata gatcccatcc 540

-continued

aaagtgtcaa ggggaaagtt gtcattgatg catttcgcct tattaaccct cagaccatga 600

tgcttggtca ggagccacga cagacaacat caaatgttgg gcacctaaat aagccatcta 660

ttcaggctct tattcatggg ctgaacaggc actactattc aattgcaatc aattaccgga 720

aaaatgagct tgaggaaaag atgttactga acttgcacaa aaagaaatgg accgatggat 780

tgattctgaa gaggtttgac actcattcaa agaccaatga gcagactgtt caggaaatgc 840

tgaaccttgc tatcaagtac aacaaggcgg tgcaagagga ggatgagctg ccgcctgaga 900

aattagcgat agcaaatgtg ggacggcaag atgctaagaa gcacttggaa gagcatgtct 960

ccaatttgat gtcatcaaac atagttcaga cgctaggaac catgctcgat acagttgtat 1020

tttagatcac tactgctgtt atcccaacac tgtacccaga gctcgtttat tttttatttt 1080

tttatgttta tcgaagccta ccataattca gtgaacttaa cgccagttac atttgggtta 1140

tgaaagctta ccacttgaca acttcat 1167

<210> SEQ ID NO 34
<211> LENGTH: 871
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: TC90038 (PRO0117)

<400> SEQUENCE: 34

cctagctcct cccgccgccg ccgccgccgc cgccgccgcc tctccactcg agagacccag 60

ccgccgccgc cgccgccgcc gccatgtcgc tgatcgccgg ggaggacttc cagcacatcc 120

tgcgtctgct gaacaccaac gtcgatggga agcagaagat catgttcgcg ctcacctcca 180

tcaagggtgt cggccgcagg ttctccaaca tcgcctgcaa gaaggccgac atcgacatga 240

acaagagggc cggtgagctt acgccggagg agctggagcg gctgatgacc gtggtggcga 300

acccgcggca gttcaaggtg cccgactggt tcctcaacag gaagaaggac tacaaggacg 360

ggaggttctc ccaggttgtc tccaacgcgc tcgacatgaa gctcagggat gatcttgaga 420

ggctcaagaa gatcaggaac caccgtggtc tgaggcacta ctggggcctc cgtgtgcgtg 480

ggcagcacac caagacaacc ggaaggaggg gtaagactgt cggtgtgtcc aagaagcgat 540

aagcctaaga accacccgag acttgatgaa gcgtttcgtt gggtgatgtt ttgccctagg 600

ataatatttt gcagctatgg aaccttgtcg taatgtatct tgaagagtgt ctttgggaac 660

taagagtaat ttacttttct tgaaactatt gcagtattga ctccttgttt attgcttttc 720

tccactttct tctacccact taaaactatt gcagtatcga ctccttgttt attgctattc 780

tccactggct tctgccttaa ttttggatgt tgcatgcgct gtgtatctgg ttcatgtgat 840

gtacccatgg cagctttgat gcattgggat t 871

<210> SEQ ID NO 35
<211> LENGTH: 1245
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: TC82936 (PRO0122)

<400> SEQUENCE: 35

acgcggccaa aacgtaccct tgtgactaca cccgcttcgc ttcctcccct ctctaagccg 60

gggaagctaa gccatggcgt ccgtcaccgc ccgcaccccg gtcgcagccc tccgctcgtc 120

ggcgtcgctc aagtctacct tcctagggca atcctccacc cgcctcgccc gcgcaccgac 180

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tacgaggcgt aatgttcggg cggaggccaa gggagagtgg ctccccggcc tcccttctcc 240

cacctacctc aacggcagct tgccaggcga taacgggttc gacccgttgg gtctggcgga 300

ggacccggag aacctgcggt ggttcgtgca ggcggagtgg tgaacgggcg gtgggcgatg 360

ctgggggtgg ccgggatgct gctgcctgag gtgctgacga agatcgggtt gatcgacgcg 420

ccgcagtggt acgacgccgg caaggccacc tacttcgcgt cgtcgtcgac gctgttcgtc 480

atcgagttca tcctgttcca ctacgtggag atccggcggt ggcaggacat caagaaccct 540

ggctgcgtca accaggaccc catcttcaag agctacagcc tcccgccgca cgagtgcggc 600

taccccggca gcgtcttcaa ccccctcaac ttcgagccca ccctcgaggc caaggagaag 660

gagctcgcca acgggaggct ggcgatgctg gcgttcttgg ggttcctggt gcagcacaac 720

gtgacgcaga aggggccctt cgacaacctg ctgcagcacc tgtctgaccc gtggcacaac 780

accatcatcc agacgctgtc aggctgagcg tgtgatcgat ttcatcaggg ccagggcatc 840

tcaaggagct tgatgagttc aggctggtga aaccgatgat tgggcgatgg aagatgttct 900

cttcttgttt cttctttttt tttttgtgga gtatgcatgt ataagatgtt aatgaattgg 960

ggggaggaga gagagagaga tggatgtgat gagattcaga cttactgtgt gtgttgtggt 1020

aattgtttcc tgcatgcatg gatctggatg catgggtgag ggggtgagtt gagtggtgaa 1080

tttctgatgt acagtactac agggggataa actatctcat ggtagcagca gtgttctagc 1140

tatctcatgg tctcgatctt aattatggtg gataaactac gcttaattgc ttgtcaagtg 1200

cttcatttgc gcattgattc agtattgcgt atcgattcaa agacc 1245

<210> SEQ ID NO 36
<211> LENGTH: 1416
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: TC89839 (PRO0123)

<400> SEQUENCE: 36

cccacgcgtc cgcccacgcg tccgggacac cagaaacata gtacacttga gctcactcca 60

aactcaaaca ctcacaccaa tggctctcca agttcaggcc gcactcctgc cctctgctct 120

ctctgtcccc aagaagggta acttgagcgc ggtggtgaag gagccggggt tccttagcgt 180

gagcagaagg ccaagaagcc gtcgctggtg gtgagggcgg tggcgacgcg gcgggccggt 240

ggcgagcccc ggcgcgggca cgtcgaaggc ggacgggaag aagacgctgc ggcaggggggt 300

ggtggtgatc accggcgcgt cgtcggggct cgggctcgcg gcggcgaagg cgcttggcgg 360

agacggggaa gtggcacgtg gtgatggcgt tccgcgactt tcctgaaggc ggcgacggcg 420

gcgaaggcgg cggggatggc ggcggggagc tacaccgtca tgcacctgga cctcgcctcc 480

ctcgacagcg tccgccagtt cgtggacaac ttccggcgct ccggcatgcc gctcgacgcg 540

ctggtgtgca acgccgcaca tctaccggcc gacggcgcgg caaccgacgt tcaacgccga 600

cgggtacgag atgagcgtcg gggtgaacca cctgggccac ttcctcctcg cccgcctcat 660

gctcgacgac ctcaagaaat ccgactaccc gtcgcggcgg ctcatcatcc tcggctccat 720

caccggcaac accaacacct tcgccggcaa cgtccctccc aaggccgggc taggcgacct 780

ccgggggctc gccggcgggc tccgcgggca gaacgggtcg gcgatgatcg acggcgcgga 840

gagcttcgac ggcgccaagg cgtacaagga cagcaagatc tgtaacatgc tgacgatgca 900

ggagttccac cggagattcc acgaggagac cgggatcacg ttcgcgtcgc tgtacccggg 960

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gccgttccag cggttcgtga cgaaggggtt cgtgtcggag gcggagtccg ggaagcggct 1080

ggcgcaggtg gtgggcgacc cgagcctgac caagtccggc gtgtactgga gctggaacaa 1140

ggactcggcg tcgttcgaga accagctctc gcaggaggcc agcgacccgg agaaggccag 1200

gaagctctgg gacctcagcg agaagctcgt cggcctcgtc tgagtttatt atttacccat 1260

tcgtttcaac tgttaatttc ttcggggttt agggggtttc agctttcagt gagagaggcc 1320

tgtcaagtga tgtacaatta gtaatttttt tttacccgac aaatcatgca ataaaaccac 1380

aggcttacat tatcgatttg tccacctaaa ttaagt 1416

<210> SEQ ID NO 37
<211> LENGTH: 1149
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: TC85888 (PRO0133)

<400> SEQUENCE: 37

cttctacttc tatcatacca aacaaactag cttaatttgc attgcatcac attgccggcc 60

gccatgagag ctctcgctct cgcggtggtg gccatggcgg tggtggccgt gcgcggcgag 120

cagtgcggca gccaggccgg cggcgcgctc tgccccaact gcctctgctg cagccagtac 180

ggctggtgcg gctccacctc cgattactgc ggcgccggct gccagagcca gtgctccggc 240

ggctgcggcg gcggcccgac cccgccctcc agcggtggcg gcagcggcgt cgcctccatc 300

atatcgccct cgctcttcga ccagatgctg ctccaccgca acgaccaggc gtgcgccgct 360

aagggcttct acacctacga cgccttcgtc gccgccgcca acgcctaccc ggacttcgcc 420

accacccgcg acgccgacac ctgcaagcgc gaggtcgccg ccttcctggc gcagacgtcc 480

cacgagacca ccggcggctg gcccacggcg cccgacggcc cctactcctg gggctactgc 540

ttcaaggagg agaacaacgg caacgccccc acatactgcg agcccaagcc ggagtggccg 600

tgcgccgccg cgaagaagta ctacggccgg ggacccatcc agatcaccta caactacaac 660

tacggccgcg gggcaggcat cggctccgac ctgctcaaca acccggacct ggtggcgtcg 720

gacgccagtc tccttcaaga cggcgttctg gttctggatg acgccgcagt cgcccaagcc 780

gtcgtgccac gcggtgatca ccggccagtg gacgccgtcc gccgacgacc aggcggcggg 840

gcgcgttccg ggctacggcg agatcaccaa catcatcaac ggcggtgtgg agtgcgggca 900

cggcgcggac gacaaggtgg ccgaccggat cgggttctac aagcgctact gcgacatgct 960

gggcgtcagc tatggcgata acctggattg ctacaaccag aggccctacc cgccttccta 1020

gttgatattt gatccgagca gacgaataaa atacaatgca cacgagattg tgagactcga 1080

gaaaacatat actacctctg aattttaata catatctcta aaacaaaaaa aaaaaaaaaa 1140

aaaatatac 1149

<210> SEQ ID NO 38
<211> LENGTH: 981
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: TC84300 (PRO0151)

<400> SEQUENCE: 38

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aagaggcaag agcatccgta ttaaccagcc ttttgagact tgagagtgtg tgtgactcga 60

tccagcgtag tttcagttcg tgtgttggtg agtgattcca gccaagtttg cgatggcttc 120

tcagcaggaa cgggctagct accacgccgg cgagaccaag gcccgcgccg aggagaagac 180

ggggcgcatg atgggcacgg cgcaggagaa ggcgcgggag gccaaggaca cggcgtccga 240

cgccgcgggg cgcgcgatgg gcaggggaca cggcgccaag gaggcgacca aggagaaggc 300

gtacgagacc aaggacgcga ccaaggagaa ggcgtacgag gcaaaggacg cggcctccga 360

cgccaccggc cgcgccatgg acaagggccg cggcgccgcg ggcgccacga gggacaaggc 420

gtacgatgcc aaggacaggg cggctgacac ggcgcagtcc gccgccgacc gcgcccgcga 480

cggcgccggg cagaccggga gctacattgg acagaccgcc gaggccgcca agcagaaagc 540

ggccggcgcc gcgcagtacg ccaaggagac cgcgatcgcc ggcaaggaca agaccggcgc 600

cgtgctccag caggcagggg agcaggtgaa gagcgtggcg gtgggggcga aggacgcggt 660

gatgtacacg ctcgggatgt caggcgataa caagaacaac gccgctgccg gcaaggacac 720

cagcacctac aagcctggaa ctgggagtga ctaccagtaa tacggtagaa gaagcatgtg 780

tcgtctttgg cactgatgcc aaagtgtacg tgttgtatcc tctttttaa gtttcagctc 840

gacttcgacg tgttcggtgt cacactttgg tttttcagtt gtgctcaact gttcatgttt 900

ctggttccat ggagggccag tgtggaggtc aatgtttaag ctttcgtttt aaaatctgat 960

aataaagttg gttaagacct g 981

<210> SEQ ID NO 39
<211> LENGTH: 1203
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: TC89687 (PRO0169)

<400> SEQUENCE: 39

tactcctctc tctcacctcc accatctagc tcactcacac agtctccact cacacgcatt 60

gcagaggaga ggcgacaatg gaggggaagg aggaggacgt gcggctgggg gcgaacaggt 120

actcggagag gcagccgata gggacggcgg cgcagggcgc gggggacgac aaggactaca 180

aggagccgcc gccgggccgc tgttcgagcc aggggagctc aagtcgtggt ctttctaccg 240

ggccgggatc gccgagttcg tcgccacctt cctcttcctc tacatcacca tcctcaccgt 300

catgggggtc tccaagtcct cctccaagtg cgccaccgtc ggcatccagg gcatcgcctg 360

gtccttcgga ggcatgatct tcgcgctcgt ctactgcacc gccggcatct ccggaggaca 420

catcaaccca gcagttactt ttgggctgtt cttggccagg aagctgtccc tgacccgggc 480

catcttctac atagtgatgc aatgcctagg ggccatctgc ggagctggag ttgtgaaggg 540

cttccagcag ggtctgtaca tgggcaatgg cggtggtgcc aatgtagttg ccagtggcta 600

caccaagggt gacggtcttg gtgctgagat tgttggcacc ttcatcctgg tctacaccgt 660

cttctcagcc actgatgcca agaggaatgc cagggactca catgttccta tccttgcccc 720

actgccaatt ggttttgcgg tgttcctggt ccacctggcc accatcccca tcaccggtac 780

tggcatcaac ccagccagga gccttggcgc tgccatcatc tacaacaagg accatgcctg 840

gaatgaccat tggatcttct gggttggtcc cttcgttggc gctgccctgg ctgccatcta 900

ccaccaggtg atcatcaggg cgatcccatt caagagcagg tcttaagccc cgcgccgccg 960

ctgcgcagcc gacgacatgc aacgcaatcg tgatgtcctg tttcccgcgc gctactgctg 1020

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cgcatctgtc gattccctct atctctagtc cccaagatgt ttttcctatc tgaaccctga 1080

acaactcaat cgtgtaatcc agtactcagt cactgtatgt ttttatgtga tggagatctt 1140

aattcttaag ttatcatctc tgttgctgga aatccggttt cctcttcgtg catgaaccgc 1200

gcc 1203

<210> SEQ ID NO 40
<211> LENGTH: 964
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: TC89846 (PRO0170)

<400> SEQUENCE: 40

cccacggttc cgcccacggt ccgcccacgg tccgcttctc ttctctggtg gtgtgggtgt 60

gtccctgtct cccctctcct tcctcctctc ctttcccctc ctctcttccc ccctctcaca 120

agagagagag cgccagactc tccccaggtg aggattcagc catgaagggg gccaaatcca 180

agggcgccgc caagcccgac gccaagttgg ctgtgaagag taagggcgcg gagaagcccg 240

ccgccaaggg caggaagggg aaggccggca aggaccccaa caagcccaag agggctccct 300

ccgctttctt cgtttttatg gaggagttcc gtaaggagtt caaggagaag aaccccaaga 360

ataaatctgt cgctgctgta ggaaaagcag ccggtgatag gtggaaatcc ctgaccgaag 420

cggacaaggc tccctatgta gccaaggcca acaagctcaa ggccgagtac aacaaggcca 480

ttgctgccta caacaagggc gagagcactg ccaagaaggc acccgccaag gaggaagagg 540

aggacgacga ggaggaatct gacaagtcca agtccgaggt caatgatgag gatgacgacg 600

agggcagcga agaggatgaa gacgatgacg agtgagcctt ccagtggaca agatgggagc 660

agcaagacgc taagggcggc gggcgtccta aggagcctat ccatcatcat catcgtctac 720

tagaattatt cagtttcact tcacatcgtg atgttttact ttttctctcg tcctataacg 780

gatagcgctc cttgttggcg ccactggtgg gtgttgtggt gcagccaatg tcttgtctcc 840

accgtcaatg atccgcttgt acctagatta ctctttccat tgtcatcggc taacattgtg 900

ataatatcag tttgcgtatg ttagattaaa ttgtttctaa ttccgtcgtt ttcttcttcc 960

ttgc 964

<210> SEQ ID NO 41
<211> LENGTH: 1542
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: TC82935 (PRO0171)

<400> SEQUENCE: 41

cacacctcac acctcaccac catcacctcc tcctcctcct cctcttcctc cgcgcgcgcg 60

agatccaggg agagggagag ggagagatca tggcggggac ggtgacggtg ccgtcggcgt 120

cggtgccgtc gacgccgctg ctcaaggacg agctggacat cgtgatcccg acgatccgca 180

acctggactt cctggagatg tggcggccct tcttccagcc ctaccacctc atcatcgtgc 240

aggacggcga cccgaccaag accatccgcg tccccgaggg cttcgactac gagctctaca 300

accgcaacga catcaaccgg atcctcggcc ccaaggcctc ctgcatctcc ttcaaggact 360

ccgcatgccg ctgcttcggc tacatggtct ccaagaagaa gtacgtcttc accatcgacg 420

acgactgctt cgttgccaag gacccatctg gcaaggacat caatgctctt gagcagcaca 480

tcaagaacct cctcagcccg tccaccccgt tcttcttcaa caccttgtat gatccctacc 540

gcgaaggcgc tgactttgtc cgtggttacc ccttcagcct cagggaggga gccaagactg 600

ctgtctctca cggcctgtgg cttaacatcc ctgactatga tgctcctact cagatggtca 660

agcctcgtga gaggaactcc aggtatgttg atgctgtcat gactgtgccc aagggaacct 720

tgttccccat gtgtggcatg aaccttgctt ttgaccgtga tctcatcggt cctgcaatgt 780

actttggtct catgggtgat ggccagccta ttggtcgcta cgacgacatg tgggctggat 840

ggtgcatgaa ggtcatctgt gaccacctga gcctgggagt gaagactgga ctgccgtaca 900

tctggcacag caaggctagc aacccttcg tgaacttgaa gaaggaatac aagggcatct 960

tctggcagga ggacatcatc cccttcttcc agaacgccac catccccaag gagtgcgaca 1020

ccgtccagaa gtgctacctc tccctcgccg agcaggtcag ggagaagctc ggcaagatcg 1080

acccctactt cgtcaagctt gccgatgcca tggtcacctg gatcgaggcc tgggatgagc 1140

tgaacccctc gactgctgct gtcgagaacg gcaaggccaa gtagattgat cctgggagct 1200

tgtgtgtcgc aggatggaaa gtacccttta agtgaaagtg ttgctgtggc ctaggccccc 1260

tagatatagc tctttttgag atgaagggag agattactta agcaacttta taattctttg 1320

ttgttatgct ggttcttttg tagctggaaa aggatttgtt atcatcgttt acataattca 1380

agacaataat aattttatca tgtaattttg atagtcgtgc tttggttgct aaatggtgtt 1440

attgtattta ataacctttg caaatcacta tacctgttgg ttgttctgag aattgtatgc 1500

actaccatat tatatttcta aatcatttcg taggcattat gg 1542

<210> SEQ ID NO 42
<211> LENGTH: 1432
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: TC82977 (PRO0173)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1429)..(1429)
<223> OTHER INFORMATION: n = any nucleotide

<400> SEQUENCE: 42

aaaagagcag cgtcgcctct cctcctccct aacccctacg cttccagaac cttctcgaag 60

ctcccgctcc ccccccccct ccgctccaat ggcgaaggaa ccgatgcgcg tgctcgtcac 120

cggcgccgca ggacaaattg gatatgctct tgtccccatg attgctaggg gtgtgatgtt 180

gggtgctgac cagcctgtta ttctacacat gcttgacatt ccaccagcta ctgaatctct 240

taatggcctt aagatggagc tggttgatgc tgcatttcct cttttgaagg gaattgtcgc 300

aacaactgat gttgtggagg cctgcactgg tgtgaatgtt gcggttatgg ttggtgggtt 360

ccccaggaag gagggaatgg aaaggaagga tgttatgtca aaaaatgtct ccatctacaa 420

atcccaagct tctgctcttg aggctcatgc agcccctaac tgcaaggttc tggtagttgc 480

caatccagca aacaccaacg ctctcatctt aaaagaattc gctccatcca tccctgagaa 540

gaacattact tgcctcaccc gtcttgacca caacagggca cttggccaga tctctgaaaa 600

acttaatgtc caagttactg atgtgaagaa tgcgatcatc tggggcaacc actcatccac 660

ccagtaccct gatgttaacc acgccactgt gaagactccc agtggagaga agcctgtcag 720

ggaactcgtt gctgatgatg agtggttaaa tacggaattc atctctaccg tccagcagcg 780

tggtgccgcc atcatcaagg cgaggaagca atccagtgcc ctatctgctg ccagctctgc 840

atgcgatcac attcgtgact gggttcttgg cactcctgag ggaacatttg tctccatggg 900

tgtgtactct gatggttcgt atggtgtgcc tgctggtctg atctactcgt tcccagtaac 960

atgcagtggt ggcgaatgga cgattgttca gggtctcccg atcgacgagt tctcaaggaa 1020

gaagatggac gcgactgccc aggagctgtc ggaggagaag acgctcgctt actcatgcct 1080

caactaaaac taagcaatac ccagagggac agatagtgag cgattgcccg ctcccgtgtt 1140

tttgaataaa agagactttt aagttccatc acatagaaac tgtttatctc agaccgctgc 1200

acatcgcgag atgtggagcg cagatgccgt tgctggtttt actccagtgt gtattgaggc 1260

tttgtactag ctccctttt tttgcctggt gattcgcagg acatttgctg aaaacattga 1320

acccatttga catctgatgg aatcatggac cagtagcaag tacatttttg cgaaagcata 1380

atctgcatcg ggcttgggct ggtggttgaa ctttctgcca catggcccnt gg 1432

<210> SEQ ID NO 43
<211> LENGTH: 659
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: TC83646 (PRO0175)

<400> SEQUENCE: 43

gctaagtgag ctagccactg atcagaagaa cacctcgatc tctgagagtg ttttttcagc 60

tttagcttaa gcaggatgga gcaccagggg cagcacggcc acgtgaccag ccgcgtcgac 120

gagtacggca acccggtcgg caccggcgcc ggacacggcc agatgggcac cgccggcatg 180

gggacgcacg gcaccgccgg caccggcggc ggccagttcc agccgatgag ggaggagcac 240

aagaccggcg gcgtcctgca acgctccggc agctccagct caagctcgtc tgaggatgat 300

ggaatgggag ggaggaggaa gaaggggatc aaggagaaga tcaaggagaa gctccccggc 360

ggcaacaagg gcgagcagca gcatgccatg ggcggcaccg gcaccggcac cggcaccggc 420

accggaaccg gcggcgccta cgggcagcag ggccacggca ccgggatgac caccggcacc 480

accggcgcac acggcaccac caccaccgac accggcgaga agaagggcat catggacaag 540

atcaaggaga agctgcccgg ccagcactga gctcgacaca ccaccacacc atgtgtctgc 600

gcccccggcg accgccgcca cgtcaccttc ctgaataata agatgagcta accgagcgc 659

<210> SEQ ID NO 44
<211> LENGTH: 1310
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: TC90619 (PRO0177)

<400> SEQUENCE: 44

ggaccagcga gcaaccagcc ccccgccccc aatggcggca gagcagcttt gcccaccgct 60

gccgcttttg cccacctctc ctccgattaa tcccctcccc tcctcttcct cccacttctc 120

cgcctcctct tcctcccctc gccgacccta cctactcgcg ccgccgccgt cgcattgggc 180

ggcaaacgga gggggggtta accctgatgg agcagtacga gaaggaggag aagattgggg 240

agggcacgta cggggtggtg tacagggcgc gggacaaggt caccaacgag acgatcgcgc 300

tcaagaagat ccggcttgag caggaggatg agggcgtccc ctccaccgca atccgcgaga 360

tctcgctcct caaggagatg catcacggca acatcgtcag gttacacgat gttatccaca 420

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gtgagaagcg catatatctt gtctttgagt atctggatct ggacctaaag aagttcatgg 480

actcttgtcc agagtttgcg aaaaacccca ctttaattaa gtcatatctc tatcagatac 540

tccgcggcgt tgcttactgt cattctcata gagttcttca tcgagatttg aaacctcaga 600

atttattgat agatcggcgt actaatgcac tgaagcttgc agactttggt ttagccaggg 660

catttggaat tcctgtccgc acgtttactc acgaggttgt aaccttgtgg tatagagctc 720

cagagatcct tcttggatca aggcagtatt ctacaccagt tgatatgtgg tcagttggtt 780

gtatctttgc agaaatggtg aaccagaaac cactgttccc tggtgattct gagattgatg 840

aattatttaa gatattcagg gtactaggaa ctccaaatga acaaagttgg ccaggagtta 900

gctcattacc tgactacaag tctgctttcc ccaagtggca agcacaggat cttgcaacta 960

ttgtccctac tcttgaccct gctggtttgg accttctctc taaaatgctt cggtacgagc 1020

caaacaaaag gatcacagct agacaggctc ttgagcatga atacttcaag gaccttgaga 1080

tggtacaatg accctgctat ggctttacat tggattggca tatgtatggg ctgggctcct 1140

catttcattc cttctgtgaa cgctgtgccc ttcgtttggg catttttgtc attcagctgg 1200

atatttcaaa tcttgtgtgt ttgatatgta ttcaggaacg ctaaatagat caccgtcttg 1260

gtctctattt gttcagagta aatatcttcc aatgctgcct ttcagtttcc 1310

<210> SEQ ID NO 45
<211> LENGTH: 55
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: prm3780

<400> SEQUENCE: 45

ggggacaagt ttgtacaaaa aagcaggctt cgacgctact caagtggtgg gaggc 55

<210> SEQ ID NO 46
<211> LENGTH: 55
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: prm2768

<400> SEQUENCE: 46

ggggacaagt ttgtacaaaa aagcaggctc ccgatttagt agaccacatt ttggc 55

<210> SEQ ID NO 47
<211> LENGTH: 54
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: prm2420

<400> SEQUENCE: 47

ggggacaagt ttgtacaaaa aagcaggcta tgccatcgag tggtgtgccg atac 54

<210> SEQ ID NO 48
<211> LENGTH: 54
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: prm2853

<400> SEQUENCE: 48

ggggacaagt ttgtacaaaa aagcaggctt ctcttctgaa gctgaagccc tgcg 54

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<210> SEQ ID NO 49
<211> LENGTH: 53
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: prm2426

<400> SEQUENCE: 49

ggggacaagt ttgtacaaaa aagcaggcta aaaccaccga gggacctgat ctg 53

<210> SEQ ID NO 50
<211> LENGTH: 55
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: prm2855

<400> SEQUENCE: 50

ggggacaagt ttgtacaaaa aagcaggctc ctagctatat gcagaggttg acagg 55

<210> SEQ ID NO 51
<211> LENGTH: 53
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: prm3025

<400> SEQUENCE: 51

ggggacaagt ttgtacaaaa aagcaggcta tggtgccatg tcaataagac atc 53

<210> SEQ ID NO 52
<211> LENGTH: 56
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: prm3029

<400> SEQUENCE: 52

ggggacaagt ttgtacaaaa aagcaggctg tttttctatg aaccggtcat taaacc 56

<210> SEQ ID NO 53
<211> LENGTH: 55
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: prm3061

<400> SEQUENCE: 53

ggggacaagt ttgtacaaaa aagcaggctc ctgatggatg atgaatcact gatcg 55

<210> SEQ ID NO 54
<211> LENGTH: 57
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: prm3031

<400> SEQUENCE: 54

ggggacaagt ttgtacaaaa aagcaggctt cgttaagttt gatgatttct gatgacc 57

<210> SEQ ID NO 55
<211> LENGTH: 53
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: prm3051

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<400> SEQUENCE: 55

ggggaccact ttgtacaaga aagctgggtg ccgccgctcg ctcgcttcgt tcg 53

<210> SEQ ID NO 56
<211> LENGTH: 58
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: prm3592

<400> SEQUENCE: 56

ggggacaagt ttgtacaaaa aagcaggctc gtgttcatgt tcgcatttag gattggac 58

<210> SEQ ID NO 57
<211> LENGTH: 55
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: prm5131

<400> SEQUENCE: 57

ggggacaagt ttgtacaaaa aagcaggctc agatgccaca gtatggtgta ccacc 55

<210> SEQ ID NO 58
<211> LENGTH: 56
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: prm3782

<400> SEQUENCE: 58

ggggacaagt ttgtacaaaa aagcaggctt tgcagttgtg accaagtaag ctgagc 56

<210> SEQ ID NO 59
<211> LENGTH: 54
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: prm2844

<400> SEQUENCE: 59

ggggacaagt ttgtacaaaa aagcaggctt ttggcgcggg gcagaagagt ggac 54

<210> SEQ ID NO 60
<211> LENGTH: 57
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: prm2973

<400> SEQUENCE: 60

ggggacaagt ttgtacaaaa aagcaggctg cttgagtcat agggagaaaa caaatcg 57

<210> SEQ ID NO 61
<211> LENGTH: 53
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: prm3770

<400> SEQUENCE: 61

ggggacaagt ttgtacaaaa aagcaggctc gtcctccttt tgtaacggct cgc 53

<210> SEQ ID NO 62
<211> LENGTH: 56

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<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: prm3772

<400> SEQUENCE: 62

ggggacaagt ttgtacaaaa aagcaggctc atgcggctaa tgtagatgct cactgc 56

<210> SEQ ID NO 63
<211> LENGTH: 53
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: prm3774

<400> SEQUENCE: 63

ggggacaagt ttgtacaaaa aagcaggctt agtaccattc ttccctcgtg agc 53

<210> SEQ ID NO 64
<211> LENGTH: 53
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: pm3776

<400> SEQUENCE: 64

ggggacaagt ttgtacaaaa aagcaggctg tttggttggt gaccgcaatt tgc 53

<210> SEQ ID NO 65
<211> LENGTH: 55
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: prm3800

<400> SEQUENCE: 65

ggggacaagt ttgtacaaaa aagcaggctg tcaccaccgt catgtacgag gctgc 55

<210> SEQ ID NO 66
<211> LENGTH: 55
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: prm5135

<400> SEQUENCE: 66

ggggacaagt ttgtacaaaa aagcaggctc agacacctag aatatagaca ttccc 55

<210> SEQ ID NO 67
<211> LENGTH: 55
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: prm3781

<400> SEQUENCE: 67

ggggaccact ttgtacaaga aagctgggtg atcacaagcg cagctaatca ctagc 55

<210> SEQ ID NO 68
<211> LENGTH: 57
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: prm2769

<400> SEQUENCE: 68

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ggggaccact ttgtacaaga aagctgggtc gtgtagaaaa tcttaacccg aaaatcg 57

<210> SEQ ID NO 69
<211> LENGTH: 55
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: prm2421

<400> SEQUENCE: 69

ggggaccact ttgtacaaga aagctgggtg gtgaggtgcc ggggaagcga cgttg 55

<210> SEQ ID NO 70
<211> LENGTH: 54
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: prm2854

<400> SEQUENCE: 70

ggggaccact ttgtacaaga aagctgggtt tcttctttcc cttggaacta accg 54

<210> SEQ ID NO 71
<211> LENGTH: 54
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: prm2427

<400> SEQUENCE: 71

ggggaccact ttgtacaaga aagctgggtt gtcgctttta tttggcttgg tgtg 54

<210> SEQ ID NO 72
<211> LENGTH: 56
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: prm2856

<400> SEQUENCE: 72

ggggaccact ttgtacaaga aagctgggtc tctagctcga tctctcttgc aaaagc 56

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<400> SEQUENCE: 73

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<210> SEQ ID NO 75
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<212> TYPE: DNA
<213> ORGANISM: Artificial sequence

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<220> FEATURE:
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ggggaccact ttgtacaaga aagctgggta ttgtgtaaat atttctattg tccagtaatc 60

ac 62

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ggggaccact ttgtacaaga aagctgggtg atggcagagt taattagcaa acgc 54

<210> SEQ ID NO 77
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<212> TYPE: DNA
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<220> FEATURE:
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<400> SEQUENCE: 77

ggggacaagt ttgtacaaaa aagcaggctc taagggcagc agccattggg 50

<210> SEQ ID NO 78
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<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: prm3049

<400> SEQUENCE: 78

ggggaccact ttgtacaaga aagctgggtg gcggcggcgg cggcggcggc ggctgggtct 60

<210> SEQ ID NO 79
<211> LENGTH: 54
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
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<400> SEQUENCE: 79

ggggaccact ttgtacaaga aagctgggtc ggcttagaga ggggaggaag cgaa 54

<210> SEQ ID NO 80
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<212> TYPE: DNA
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<220> FEATURE:
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<400> SEQUENCE: 80

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<210> SEQ ID NO 81
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<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
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<400> SEQUENCE: 81

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ggggaccact ttgtacaaga aagctgggtc ggcaatgtga tgcaatgcaa attaagc 57

<210> SEQ ID NO 82
<211> LENGTH: 55
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: prm2974

<400> SEQUENCE: 82

ggggaccact ttgtacaaga aagctgggtc gcaaacttgg ctggaatcac tcacc 55

<210> SEQ ID NO 83
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<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
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<400> SEQUENCE: 83

ggggaccact ttgtacaaga aagctgggtt gtcgcctctc ctctgcaatg cgtg 54

<210> SEQ ID NO 84
<211> LENGTH: 52
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
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<400> SEQUENCE: 84

ggggaccact ttgtacaaga aagctgggtg gctgaatcct gcgagaaggg cg 52

<210> SEQ ID NO 85
<211> LENGTH: 54
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
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<400> SEQUENCE: 85

ggggaccact ttgtacaaga aagctgggtg atctctccct ctccctctcc ctgg 54

<210> SEQ ID NO 86
<211> LENGTH: 52
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
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<400> SEQUENCE: 86

ggggaccact ttgtacaaga aagctgggtt ggagcggaag ggggggggga gc 52

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<211> LENGTH: 57
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: prm3801

<400> SEQUENCE: 87

ggggaccact ttgtacaaga aagctgggtc actctcagag atcgaggtgt tcttctg 57

<210> SEQ ID NO 88
<211> LENGTH: 52
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence

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<220> FEATURE:
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<400> SEQUENCE: 88

ggggaccact ttgtacaaga aagctgggtc gcccgcagct cgcccccgtc cg 52

We claim:

1. A method for driving leaf-preferable expression of a nucleic acid in a plant comprising introducing into a cell of a monocot or dicot plant a genetic construct comprising (a) an isolated promoter comprising an isolated nucleic acid comprising the sequence of SEQ ID NO: 14; and (b) a heterologous nucleic acid sequence operably linked to said isolated promoter; and optionally (c) a 3' transcription terminator, and

testing and selecting a transgenic plant with leaf-preferable expression of said heterologous nucleic acid sequence.

2. The method according to claim 1, wherein after said introducing step and prior to said testing and selecting step, said cell of a monocot or dicot plant is cultivated under conditions promoting plant growth.

3. The method according to claim 2, wherein said cell of a monocot or dicot plant is selected from the group consisting of rice, maize, wheat, barley, millet, oats, rye, sorghum, soybean, sunflower, canola, sugarcane, alfalfa, bean, pea, flax, lupinus, rapeseed, tobacco, tomato, potato, squash, papaya, poplar and cotton.

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